

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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> 0 <
O| 0 IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq2-seq4.res made by jdelaval on Tue 15 Mar 105 10:47:43 PST.

Query sequence being compared: US-10-693-367-14 (1-89)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-693-367-14 (1-89) with:
File: seq2.pep

```

100-
-
N
U 50-
M
B
E
R
O
F 10-
S
E 5-
U
N
E
C
E
S
0
SCORE 0 9 19 28 37 47 56 65 75 84
STDDEV

```

PARAMETERS

Similarity matrix Unitary 1 K-tuple 2
Mismatch penalty 1.00 Joining penalty 20
Gap penalty 0.05 Window size 32
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 84 Median 0 Standard Deviation 0.00

Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 591
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Score	Sig. Frame
1. US-10-693-367-2	Sequence 2, Application US	591	84	85	0.00 0

1. US-10-693-367-14 (1-89)

US-10-693-367-2 Sequence 2, Application US/10693367

Sequence 2, Application US/10693367

GENERAL INFORMATION:

APPLICANT: The Trustees of Columbia University

APPLICANT: Minden, Audrey

TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE

FILE REFERENCE: 575/55311-A-PCT-US

CURRENT APPLICATION NUMBER: US/10/693,367

CURRENT FILING DATE: 2003-10-24

PRIOR APPLICATION NUMBER: US/09/718,032

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: PCT/US99/11341

PRIOR FILING DATE: 1998-05-21

PRIOR APPLICATION NUMBER: 09/082,737

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 591

TYPE: PRT

ORGANISM: human

Initial Score = 84 Optimized Score = 85 Significance = 0.00
Residue Identity = 95% Matches = 85 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

MEGKRKKRYEISAPSNFBRVHTGPDHOKFTGUPROWQSILIESARPKPLVDPACITSIQPGAPKTIIVR
10 20 30 40 50 60 70

GSKGAQDGLTLLDDEFENMSTVRNSLRDRSPPPARARQENGMPEEPATTAARGPGAGSRGPRAGHSEA
80 90 100 110 120 130 140

GGSGDRRRAGPEKPKSRREGSGGPOESSRDKRPLSGPDVGPQAGIAGAKLAGRPFTYPRADTDHP
150 160 170 180 190 200 210

SRGAGCEPHDVA PNGPSAGGLAIPSSSSSSSRPPTRGARGPSRGVLGPHASBPOLAPACTPAAVAVPPPG
220 230 240 250 260 270 280

PPSPQREPORVSHQPRALQGVDPGDPRSYLDNFIKIGSGSTGIVCIATVRSQKLVAVYKMDLRKQORR
290 300 310 320 330 340 350 360

ELTFNEVIMRDYQHEHNVVENNSTYVGDDELVWMEFEGGALTDIVTTRANNEQIAAVCLAVIQALAVLH
10 20 30 40 50 60 70

ELTFNEVIMRDYQHEHNVVENNSTYVGDDELVWMEFEGGALTDIVTTRANNEQIAAVCLAVIQALAVLH
80 90 100 110 120 130 140

ACGVTHSDIKTD
150 160 170 180 190 200 210

ACGVTHSDIKTD
220 230 240 250 260 270 280

ACGVTHSDIKTD
250 260 270 280 290 300 310 320 330 340 350 360

ACGVTHSDIKTD
320 330 340 350 360 370 380 390 400 410 420 430

ACGVTHSDIKTD
400 410 420 430 440 450 460 470 480 490 500

ACGVTHSDIKTD
470 480 490 500 510 520 530 540 550 560 570 580 590

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 11:16:56 ; Search time 6.675 Seconds

(without alignments)
1282.890 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452
Sequence: 1 KQRRRLFNENVIMRDYH.....LQALAVLHAQGVTHSDIKTD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	67.0	540	2 T19956	hypothetical prote
2	303	67.0	542	2 T19952	hypothetical prote
3	277	61.3	544	2 S40482	serine/threonine-s
4	277	61.3	545	2 G01773	p21-activated proc
5	276	61.1	544	2 A57597	beta-p21-activated
6	269	59.5	544	2 T49376	p21 activated kina
7	266	58.8	622	2 T15467	hypothetical prote
8	265.5	58.7	525	2 S58682	protein kinase, p2
9	256	56.6	1230	2 T18256	probable serine/th
10	256	56.6	1230	2 T18259	serine/threonine p
11	255	56.4	939	2 S28394	probable serine/ch
12	235.5	52.1	378	2 T26684	hypothetical prote
13	231.5	51.2	842	2 S60402	protein kinase CLA
14	221	51.1	658	2 T39500	serine/threonine-s
15	221	50.2	658	2 S60170	protein kinase Pak
16	220.5	48.8	589	2 T38086	serine/threonine-p
17	203.5	45.0	655	2 S51884	probable protein k
18	177.5	39.3	819	2 A53714	protein kinase (EC
19	167.5	37.1	829	2 T29372	hypothetical prote
20	154	34.1	829	2 J06316	probable protein k
21	153	33.8	836	2 B96716	probable serine/ch
22	151.5	33.5	1401	2 T39225	MAP kinase kinase
23	149.5	33.1	545	2 T33748	hypothetical prote
24	148.5	32.9	652	2 T39722	serine/threonine p
25	146.5	32.4	1192	2 T18611	probable serine/ch
26	146.5	32.4	1246	2 G89287	protein H39E23.1 (
27	146	32.3	1233	2 T30989	serine/threonine p
28	145.5	32.2	1075	2 T27623	hypothetical prote
29	145.5	32.2	1080	2 T27622	hypothetical prote

30	145.5	32.2	1314	2 S19488	probable membrane
31	145	32.1	471	2 T39232	probable serine th
32	144.5	32.0	348	2 T37321	Ca2+/calmodulin-de
33	143	31.6	653	2 T34356	hypothetical prote
34	142.5	31.5	690	2 C96572	protein F12M16.4 (
35	141.5	31.3	1051	1 J06051	serine/threonine-s
36	141.5	31.3	1579	2 S59801	protein kinase SSK
37	139.5	30.6	312	2 T38525	serine/threonine p
38	137.5	30.4	1062	2 S45367	protein kinase CDC
39	136	30.1	415	2 U02251	calcium/calmodulin
40	135.5	30.0	460	2 S58882	protein kinase Cdb
41	135.5	30.0	883	2 A96662	hypothetical prote
42	135	29.9	1206	2 T34021	protein kinase SK2
43	135	29.9	1231	2 T18532	serine/threonine pr
44	135	29.9	1233	2 T14157	serine/threonine p
45	133	29.4	1097	2 F96538	hypothetical prote

ALIGNMENTS

RESULT 1
T19956
hypothetical protein C45B11.1b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C:Accession: T19956
R:McMurray, A.
Submitted to the EMBL Data Library, June 1996
A:Reference number: Z19202
A:Accession: T19956
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-540 <MTL>
A:Cross-references: UNIPROT:Q9U3M1; EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C45B11
A:Experimental source: clone C45B11
C:Genetic:
A:Gene: CESP:C45B11.1b
A:Map position: 5
A:introns: 13/2; 104/2; 231/3; 367/2; 468/3
C:Superfamily: protein kinase homology

Query Match
Best Local Similarity 67.0%; Score 303; DB 2; Length 540;
Matches 60; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 KQRRRLFNENVIMRDYHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHRMNE 60
DB 284 KQRRRLFNENVISLRQYHPVIVRPFSSHLVDDELVMVMEFGSLTDIVATRMTEP 343
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 344 QIATTSRQVGLADFLHARKVIHRDKSPD 372

RESULT 2
T19952
hypothetical protein C45B11.1a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C:Accession: T19952
R:McMurray, A.
Submitted to the EMBL Data Library, June 1996
A:Reference number: Z19202
A:Accession: T19952
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <MTL>
A:Cross-references: UNIPROT:Q18617; EMBL:Z74029; PIDN:CAA98429.1; GSPDB:GN00023; CESP:C45B11
A:Experimental source: clone C45B11
C:Genetic:
A:Gene: CESP:C45B11.1a
A:Map position: 5

RESULT 7

T15467

Hypothetical protein C09B8.7 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004

C:Accession: T15467

R:Stallier, L.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of *C. elegans* cosmid C09B8.

A:Reference number: S61138

A:Accession: T15467

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-622 <STES>

A:Cross-references: UNIPROT:Q17850; EMBL:U29612; NID:g868273; PID:g868279; PIDN:AAA6805

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP.C09B8.7

A:Introns: 107/1; 182/3; 192/1; 260/3; 291/3; 481/1; 505/3; 546/3; 570/3

C:Superfamily: protein kinase homology

Query Match 58.8%; Score 266; DB 2; Length 622;

Best local similarity 56.8%; Pred. No. 1,2e-16;

Matches 50; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 2 QQRRELLFNEVIMRDYHENVEMVNSYLVGDELVMVELEGALTDIVTHTRMNEQ 61

DB 381 QPKKELINEILVMKSNKANIYVFLDSYLCDELVMVEYLAGSLTDVVTETACMD 440

QY 62 IAAVCLAVLQALAVLHAQGVHSDIKTD 89

DB 441 IAAVCREVLQALFELHSHRVHHRDKSD 468

RESULT 8

S58682

protein kinase, p21-activated (EC 2.7.1.-) - human

N:Alternate names: protein kinase PAK65; S6/H4 kinase

C:Species: *Homo sapiens* (man)

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004

C:Accession: S58682; S55258; S55304; S58690; A57441

R:Seill, M.; Krause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernoff, J.

submitted to the EMBL Data Library, April 1995

A:Description: Human p21-activated protein kinases regulate actin organization in mammal

A:Reference number: S58682

A:Accession: S58682

A:Molecule type: DNA

A:Residues: 1-525 <SEL>

A:Cross-references: UNIPROT:Q13177; EMBL:U24153; NID:g780807; PIDN:AAA65442.1; PID:g7808

R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 1970-1978, 1995

A:Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation

A:Reference number: S55258; PMID:95262637; PMID:7744004

A:Accession: S55258

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 'MEBQQGNSDEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525

A:Accession: S55304

A:Molecule type: protein

A:Residues: 402-418 <MA>

R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 4385, 1995

A:Reference number: S58690; PMID:96016211; PMID:7556080

A:Contents: erratum

A:Accession: S58690

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-30 <MA>

R:Benner, G.E.; Dennis, P.B.; Maesacchia, R.A.

J. Biol. Chem. 270, 21121-21128, 1995

A:Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular an

A:Reference number: A57441; PMID:95403344; PMID:7673144

A:Accession: A57441

A:Molecule type: protein

A:Residues: 197-216/402, 'S', 404-409 <BEN>

A:Experimental source: placenta

C:Superfamily: protein kinase homology

C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin

F:247-501/Domain: protein kinase homology <KIR>

F:255-263/Region: protein kinase ATP-binding motif

F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 58.7%; Score 265.5; DB 2; Length 525;

Best local similarity 57.8%; Pred. No. 1,2e-16;

Matches 52; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 KQQRRELLFNEVIMRDYHENVEMVNSYLVGDELVMVELEGALTDIVTHTRMNE 59

DB 284 QPKKELINEILVMKSNKANIYVFLDSYLCDELVMVEYLAGSLTDVVTETACMD 343

QY 60 EOIAAVCLAVLQALAVLHAQGVHSDIKTD 89

DB 344 AQIAVCREVLQALFELHSHRVHHRDKSD 373

RESULT 9

T18256

probable serine/threonine-specific protein kinase (EC 2.7.1.-) - yeast (*Candida albicans*)C:Species: *Candida albicans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18256

R:Reberer, E.; Harscus, D.; Broadbent, I.D.; Clark, K.L.; Dignard, D.; Ziegeler, K.; E

Proc. Natl. Acad. Sci. U.S.A. 93, 13217-13222, 1996

A:Title: Signal transduction through homologs of the Ste20p and Ste7p protein kinases ca

A:Reference number: Z18843; PMID:97075145; PMID:8917571

A:Accession: T18256

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1230 <LEB>

A:Cross-references: UNIPROT:Q13411; EMBL:L47210; NID:g2276410; PID:g2286042; PIDN:AA654

C:Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 56.6%; Score 256; DB 2; Length 1230;

Best local similarity 50.6%; Pred. No. 2e-15;

Matches 45; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYHENVEMVNSYLVGDELVMVELEGALTDIVTHTRMNE 60

DB 989 QPKKELINEILVMKSNKANIYVFLDSYLCDELVMVEYLAGSLTDVVTETACMD 1048

QY 61 QIAVCLAVLQALAVLHAQGVHSDIKTD 89

DB 1049 QIGVCREVLQALFELHSHRVHHRDKSD 1077

RESULT 10

T18259

serine/threonine protein kinase homolog - yeast (*Candida albicans*)C:Species: *Candida albicans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18259

R:Kohler, J.R.; Pink, G.R.

Proc. Natl. Acad. Sci. U.S.A. 93, 13223-13228, 1996

A:Title: *Candida albicans* strains heterozygous and homozygous for mutations in mitogen-

A:Reference number: Z11110; PMID:97075146; PMID:8917572

A:Accession: T18259

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1230 <KOH>

A:Cross-references: UNIPROT:Q92212; EMBL:U73457; NID:g1657953; PID:g1737181; PIDN:AA654

C:Genetics:

A:Note: CST20

Query Match 56.6%; Score 256; DB 2; Length 1230;

A/Cross-references: SGD:S0005242; MIPS:YNL298w

C/Superfamily: plectstrin repeat homology; protein kinase homology
C/Keywords: ATP; phosphotransferase
F/544-825/Domain: protein kinase homology <KIN>

Query Match	51.2%	Score 231.5;	DB 2;	Length 842;
Best Local Similarity	45.9%;	Pred. No. 2.3e-13;		
Matches 45;	Conservative 20;	Mismatches 24;	Indels 9;	Gaps 2

QY 1 KQKRELLFNEVIMRDRHENVENMYNLYL-VGDELMVMMELEGALTDIY----- 52
|||:::||:::||::|||::|||::|||::|||::|||:
DB 600 KQKRELIVNELMMDSRHKRIYNFLAAYLRITDDDLVMMVEEMEGSSLTDLIENSPIND 655

[illegible]

RESULT 14

serine/threonine-specific protein kinase (EC 2.7.1.-) pak1-shk1 - fission yeast (Schizosaccharomyces pombe)
N/Alternate names: Ste20 homologous protein kinase 1
C/Species: Schizosaccharomyces pombe

C:Accession: T39500; T45523
R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1998

A:Accession: T39500
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A: Cross-references: UNIROT:P50527; EMBL:AL034433; PIDD:CAA22347.1; GSPDB:GN00066; SPDB: A; Experimental source: strain 972h-; cosmid c1604 R; Marcus, S.

A/Reference number: Z22999
A/Accession: T45523
A/Status: preliminary; translated from GB/EMBL

A/Molecule type: DNA
A/Residue: 1-658 <MAR>
A/Cross-references: EMBL:L41552; PIDN:AAB52609.1
C/Genetics:

A:Map position: 1
A:Gene: b1m1, sfbcb1004.14c
C:Superfamily: protein kinase homology
C:Keywords: hydrolase; phosphotransferase; signal transduction

Query Match	51.1%;	Score 231;	DB 2;	Length 658;
Best Local Similarity	40.4%;	Pred. No. 1.9e-13;		
Matches 36:	Conservative 28;	Mismatches 25;	Indels 0;	Gaps 0

Oy 1 KOQRELLFNEVIMRDYRHENVEMYSYLVEDELVMMELEGALTDIVTHTRNABE 60
 : :: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 421 OODKREPTAVETIWMKSHHKNITINFDTDFEVRSSTAMMFMFBGSGTTEVAITNNNTSFC 480

QY 61 QIAVCLAVLQALAVLHAQGVHSIKTD 89
 ||||:|:|:|:|:|:|
 A81 QTAATCKRETI EGI QUT HENGTVUPDTYCD 509

RESULT 15
260170

protein kinase Pak1 - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
 C:Accession: S00170

EMBO J. 14, 5908-5919, 1995
 A1:Title: Fission yeast pek1 (+) encodes a protein kinase that interacts with Cdc42p and p115
 A1:Reference number: S60170; MUID:96112805; PMID:8646783

A;Status: preliminary

A:Residues: 1-658-<OTT>
A:Cross-references: UNIPROT:P50527; EMBL:U22371; NID:g1122910; PDBN:AAC49125.1; PID:g1112
C:Superfamily: protein kinase homology

F;384-637/Domain: protein kinase homology <KIN>
F;392-400/Region: protein kinase ATP-binding motif

Query Match	50.2%;	Score 227;	DB 2;	Length 658;
Best Local Similarity	39.3%;	Pred. No. 4.5e-13;		
Matches 35;	Conservative 29;	Mismatches 25;	Indels 0;	Gaps 0

Qy 1 KQQRRELFNEVIVMEDRYHENVEMINSYLVGDELMVMMELEGALTDIVHTIRNAEE 60
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 421 QQPKEFIVMELVAKSHHHKNIIVNFIDTFYKSSELMVMMEYRGGSLTEVTNNNTLSGC 480

QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
|||:|:|:|:|:|:|
Db 481 QIAICKETLELYSDLHNGIVHRDIKSD 509

Search completed: March 15, 2005, 11:31:25
Job time : 7.675 secs

Job time : 7.675 sec

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OM protein - protein search, using sw model

Run on: March 15, 2005, 10:58:31 ; Search time 30.1029 Seconds
(without alignment)

1513.973 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452
Sequence: 1 KQORRELFENVEVIMRDYH.....LQALAVLHAGVHSDIKTD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	443	98.0	407	2 Q8K0U2	Q8K0U2 mus musculus
2	443	98.0	593	1 PAK4_MOUSE	Q8Btw9 mus musculus
3	443	98.0	593	2 Q80Z97	Q8Btw9 mus musculus
4	443	98.0	597	2 Q6ZPX0	Q6ZPX0 mus musculus
5	436	96.5	240	2 Q8NCH5	Q8NCH5 mus musculus
6	436	96.5	438	2 Q8NDE3	Q8NDE3 mus musculus
7	436	96.5	467	2 Q9UJ58	Q9UJ58 mus musculus
8	436	96.5	501	2 Q8N4E1	Q8N4E1 mus musculus
9	436	96.5	591	1 PAK4_HUMAN	Q96013 mus musculus
10	421	93.1	650	2 Q90W62	Q90W62 xenopus lae
11	418	92.5	663	2 Q6GM11	Q6GM11 brachydanio
12	412	91.2	711	2 Q6NVJ4	Q6NVJ4 brachydanio
13	409	90.5	229	2 Q9CS71	Q9CS71 mus musculus
14	407	90.0	719	2 Q8C015	Q8C015 mus musculus
15	403	89.2	719	2 Q6RWS7	Q6RWS7 mus musculus
16	402	88.9	719	1 PAK7_HUMAN	Q9P286 mus musculus
17	402	88.9	719	2 Q8TB93	Q8TB93 mus musculus
18	399	88.3	719	2 Q8BVB0	Q8BVB0 mus musculus
19	379	83.8	681	1 PAK6_HUMAN	Q9nq5 mus musculus
20	366	81.0	558	2 Q7QCS5	Q7QCS5 anopheles g
21	366	81.0	639	1 PAKM_DROME	Q9vnx5 drosophila
22	363	81.0	540	2 Q9UJ31	Q9UJ31 caenorhabdi
23	303	67.0	542	2 Q18637	Q18637 caenorhabdi
24	283	62.6	704	2 Q24190	Q24190 drosophila
25	283	62.6	704	2 Q9VJ13	Q9VJ13 drosophila
26	280	61.9	704	2 Q7QD76	Q7QD76 anopheles g
27	279	61.7	704	2 Q24213	Q24213 drosophila
28	278	61.5	447	2 Q6PAZ2	Q6PAZ2 xenopus lae
29	277	61.3	447	2 Q6PW79	Q6PW79 mus musculus
30	277	61.3	544	1 PAK1_RAT	Q35465 rattus norv
31	277	61.3	545	1 PAK1_HUMAN	Q13153 mus musculus

32	277	61.3	545	1 PAK1_MOUSE	Q88643 mus musculus
33	277	61.3	553	2 Q75561	Q75561 mus musculus
34	277	61.3	577	2 Q6P017	Q6P017 brachydanio
35	277	61.3	577	2 Q80320	Q80320 brachydanio
36	276	61.1	544	1 PAK3_RAT	Q62829 rattus norv
37	276	61.1	544	2 Q8K1R6	Q8K1R6 mus musculus
38	276	61.1	559	1 PAK3_HUMAN	Q75914 mus musculus
39	276	61.1	559	1 PAK3_MOUSE	Q61036 mus musculus
40	276	61.1	559	1 PAK3_PANTR	Q79414 pan troglod
41	276	61.1	559	1 PAK3_PONPY	Q79413 pongo pygma
42	276	61.1	564	2 Q8AXB4	Q8AXB4 xenopus lae
43	274	60.6	524	1 PAK2_HUMAN	Q13177 mus musculus
44	274	60.6	524	1 PAK2_MOUSE	Q8C14 mus musculus
45	274	60.6	524	1 PAK2_RABIT	Q29502 oryctolagus

ALIGNMENTS

RESULT 1	ID	PRELIMINARY	PRT	407 AA.
Q8K0U2	Q8K0U2	PRELIMINARY	PRT	407 AA.
AC	Q8K0U2	01-OCT-2002 (Tremblrel. 22, Created)		
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Pak4 protein (Fragment).			
GN	Name=Pak4;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange S.J.,			
RA	Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,			
RA	Krzyszewski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,			
RT	Jones S.J., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RA	Straussberg R.L.			
RA	Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL, BC030389, AAH30389.1, -.			
DR	HSSP, Q13153, 1F3W.			
DR	MGI, MGI:1917834, Pak4.			
DR	GO, GO:0005524, F-ATP binding; IEA.			
DR	GO, GO:004674, F-protein serine/threonine kinase activity; IEA.			
DR	GO, GO:000468, P-protein amino acid phosphorylation; IEA.			
DR	InterPro, IPR001109, Kinase like.			
DR	InterPro, IPR000719, Prot_kinase.			
DR	Pfam, PF00069, Pkinase; 1.			
DR	ProDom, PD000001, Prot_kinase; 1.			
DR	SMART, SM00220, S_TKc, 1.			

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding. 1
 FT NON TER 1
 SQ SEQUENCE 407 AA; 44339 MW; 921689734DF9D710 CRC64;
 Query Match 98.0%; Score 443; DB 2; Length 407;
 Best Local Similarity 97.8%; Pred. No. 1.2e-36;
 Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KOQRELLFNEVYIMRDYHENVVEMVNSYVGDLMVWVEFLGALTDIVTTRNNEE 60
 DB 172 KOQRELLFNEVYIMRDYHENVVEMVNSYVGDLMVWVEFLGALTDIVTTRNNEE 221
 QY 61 QIAAVCLAVLQALAVLHAGQYHSIDIKTD 89
 DB 232 QIAAVCLAVLQALAVLHAGQYHSIDIKTD 260
 RESULT 2
 PAK4 MOUSE STANDARD; PRT; 593 AA.
 AC Q8BTW9;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated
 DE Kinase 4) (PAK-4).
 GN Name=PAK4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01265;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi H., Bono H., Kondo S.,
 RA Nagai K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanepin A., Matsumura H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sulstana R., Takehana Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmink L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carrinzi P., Hayatsu N.,
 RA Hironaka-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Aikawa T., Fukuda N.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kigawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaeumishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs".
 RL Nature 420:563-573(2002).
 RV [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin L.B., Toshiyuki S., Carrinzi P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale K.S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Activates the JNK pathway. Implicated in the
 CC reorganization of the actin cytoskeleton and in the formation of
 CC filopodia (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
 CC CDC42/p21 and weakly with Rac1 (By similarity).
 CC -1- PTM: Autophosphorylated when activated by CDC42/p21 (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 CRIB domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AK088512; BA040396.1; -
 DR EMBL; BC048238; AA048238.1; -
 DR HSSP; Q13153; 1P3W.
 DR WGD; MG11917834; PAK4.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000095; PAKbox/Rho-binding.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR008271; Ser/Thr. kin. AS.
 DR InterPro; IPR002290; Ser/Thr. kinase.
 DR InterPro; IPR011026; WASP_C.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00786; PBD; 1.
 DR ProDom; PD000001; Prot. kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE NEG.
 KW ATP-binding. Phosphorylation; Serine/threonine-protein kinase;
 KW Transferase.
 FT DOMAIN 11 24 CRIB.
 FT DOMAIN 25 32 Linker.
 FT DOMAIN 323 574 Protein kinase.
 FT NP_BIND 329 337 ATP (By similarity).
 FT BINDING 352 352 ATP (By similarity).
 FT ACT_SITE 442 442 Proton acceptor (By similarity).
 SQ SEQUENCE 593 AA; 64622 MW; 4AFA91DD73D4C6D5 CRC64;
 Query Match 98.0%; Score 443; DB 1; Length 593;
 Best Local Similarity 97.8%; Pred. No. 1.7e-36;
 Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KOQRELLFNEVYIMRDYHENVVEMVNSYVGDLMVWVEFLGALTDIVTTRNNEE 60
 DB 358 KOQRELLFNEVYIMRDYHENVVEMVNSYVGDLMVWVEFLGALTDIVTTRNNEE 417


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QY 61 Q1AAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 418 Q1AAVCLAVLQALAVLHAQGVHSIDIKSD 446

RESULT 3
080297 PRELIMINARY; PRT; 593 AA.
AC Q80297;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P21-activated protein kinase 4.
GN Name:PAK4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=22526742; PubMed=12529371; DOI=10.1074/jbc.M205875200;
RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;
RT "P21-activated protein kinase 4 (PAK4) interacts with the keratinocyte
RT growth factor receptor and participates in keratinocyte growth factor-
RT mediated inhibition of oxidant-induced cell death."
RL J. Biol. Chem. 278:10374-10380(2003).
DR EMBL; AY217016; AAC61496.1; -.
DR HSSP; Q13153; 1F3M.
DR MGD; MG11917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/RhoGTPase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR011026; WAF_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase.
SQ SEQUENCE 593 AA; 64666 MW; D7B3BD36706B4AP4 CRC64;

Query Match 98.0%; Score 443; DB 2; Length 593;
Best Local Similarity 97.8%; Pred. No. 1.7e-36;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 K0ORRELFNEVYIMDYHENVNEMVNSYLVGDELAVMEFLGALTDIVTHRMNE 60
DB 358 K0ORRELFNEVYIMDYHENVNEMVNSYLVGDELAVMEFLGALTDIVTHRMNE 417
QY 61 Q1AAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 418 Q1AAVCLAVLQALAVLHAQGVHSIDIKSD 446

RESULT 4
062PX0 PRELIMINARY; PRT; 597 AA.
AC 062PX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA1142 protein (Fragment).
GN Name=MKIAA1142;
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129298; BAC98108.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/RhoGTPase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR011026; WAF_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding.
FT NON TER 1
SQ SEQUENCE 597 AA; 64963 MW; 50C02613F77CCADA CRC64;

Query Match 98.0%; Score 443; DB 2; Length 597;
Best Local Similarity 97.8%; Pred. No. 1.7e-36;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 K0ORRELFNEVYIMDYHENVNEMVNSYLVGDELAVMEFLGALTDIVTHRMNE 60
DB 362 K0ORRELFNEVYIMDYHENVNEMVNSYLVGDELAVMEFLGALTDIVTHRMNE 421
QY 61 Q1AAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 422 Q1AAVCLAVLQALAVLHAQGVHSIDIKSD 450

RESULT 5
08NCH5 PRELIMINARY; PRT; 240 AA.
AC 08NCH5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ90247.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto U., Nakamatsu A., Nakamura Y., Kojima S., Nagahata K.,
RA Masudo Y., Ono T., Okano K., Yoshikawa Y., Aotsuba S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074728; BAC11166.1; -.
DR HSSP; Q13153; 1F3M.
```

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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_Kinase.
DR ProDom; PD000001; Prot_Kinase; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
SQ SEQUENCE 240 AA; 27332 MW; EC686288D4913B6 CRC64;

Query Match
Best Local Similarity 96.5%; Score 436; DB 2; Length 240;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVMRDYRHENVMNYSYVGDLMVWMEFLGGALTDIVHTHNNEE 60
DB 5 KQORRELLFNEVVMRDYRHENVMNYSYVGDLMVWMEFLGGALTDIVHTHNNEE 64
QY 61 QIAAVCLAVIQAALVLAHAGVYHSDIKTD 89
DB 65 QIAAVCLAVIQAALVLAHAGVYHSDIKSD 93

RESULT 6
Q8NDE3 PRELIMINARY; PRT; 438 AA.
ID Q8NDE3
AC Q8NDE3
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, last annotation update)
DE Hypothetical protein DKFZps47G182.
GN Name=DKFZps47G182.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX TISSUE=Brain;
RP SEQUENCE FROM N.A.
RC The German cDNA Consortium;
RA Wandt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Rodo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/Genbank/DBD databases.
DR EMBL; AL834236; CAD38914.2; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006474; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
KW ATP-binding; Hypothetical protein.
SQ SEQUENCE 438 AA; 48267 MW; 4A596BCE39883 CRC64;

Query Match
Best Local Similarity 96.5%; Score 436; DB 2; Length 438;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVMRDYRHENVMNYSYVGDLMVWMEFLGGALTDIVHTHNNEE 60
DB 203 KQORRELLFNEVVMRDYRHENVMNYSYVGDLMVWMEFLGGALTDIVHTHNNEE 262
QY 61 QIAAVCLAVIQAALVLAHAGVYHSDIKTD 89
DB 263 QIAAVCLAVIQAALVLAHAGVYHSDIKSD 291

RESULT 7
Q9ULS8 PRELIMINARY; PRT; 467 AA.
ID Q9ULS8
AC Q9ULS8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, last annotation update)
DE KIAA1142 protein (Fragment).
GN Name=KIAA1142.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hiroseawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336 (1999).
DR EMBL; AB032968; BA86456.1; -.
DR HSSP; Q3153; 1P3W.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/Rho-binding.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR011026; WASP_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding.
FT NON TER
SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5E3940 CRC64;

Query Match
Best Local Similarity 96.5%; Score 436; DB 2; Length 467;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORRELLFNEVVMRDYRHENVMNYSYVGDLMVWMEFLGGALTDIVHTHNNEE 60
DB 232 KQORRELLFNEVVMRDYRHENVMNYSYVGDLMVWMEFLGGALTDIVHTHNNEE 291
QY 61 QIAAVCLAVIQAALVLAHAGVYHSDIKTD 89
DB 292 QIAAVCLAVIQAALVLAHAGVYHSDIKSD 320

RESULT 8
Q8N4E1 PRELIMINARY; PRT; 501 AA.
ID Q8N4E1
AC Q8N4E1
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, last annotation update)
DE PMK4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Ruben G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.T.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywniński M.I., Skalska U., Smalitz D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034511; AAH34511.1; -.
 DR HSSP; Q13153; 1F3M.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004674; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000095; PAKbox/RhoGAP.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR011026; WASP_C.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding.
 SQ SEQUENCE 501 AA; 54940 MW; 6EE6240EC65E79D CRC64;
 Query Match 96.5%; Score 436; DB 2; Length 501;
 Best Local Similarity 95.5%; Pred. No. 7,4e-36;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KOORRELLFENVVIMDRHENVVEMNSYLVDGLVWVEFLGALTDIVHTNNNEE 60
 DB 266 KOORRELLFENVVIMDRHENVVEMNSYLVDGLVWVEFLGALTDIVHTNNNEE 325
 QY 61 QIAVCLAVYQALAVYHAQSVIHSDIKTD 89
 DB 326 QIAVCLAVYQALVSLVLAQGVHHRDIKSD 354
 RESULT 9
 PAK4_HUMAN STANDARD; PRT; 591 AA.
 AC 096013; Q9BUJ3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated
 DE kinase 4) (PAK-4).
 GN Name=PAK4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99043860; PubMed=982598; DOI=10.1093/emboj/17.22.6527;
 RA Abo A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V.,
 RA Bellisle B., Minden A.;
 RT "PAK4, a novel effector for Cdc42Hs, is implicated in the
 RT reorganization of the actin cytoskeleton and in the formation of
 RT filopodia.";
 RL EMBO J. 17:6527-6540(1998).
 RN RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Melnick M.B.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Eye, Pancreas, and Placenta;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helen F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussid T.B., Tohyuki S., Carninci P., Prange S.J.,
 RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Millaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywniński M.I., Skalska U., Smalitz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Activates the JNK pathway. Implicated in the
 CC reorganization of the actin cytoskeleton and in the formation of
 CC filopodia.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
 CC CDC42/p21 and weakly with RAC1.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O96013-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O96013-2; Sequence=VSP_004892, VSP_004893;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Highest expression in prostate, testis and
 CC colon.
 CC -1- PTM: Autophosphorylated when activated by CDC42/p21.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 CRIB domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

 DR EMBL; AJ011855; CA09820.1; -.
 DR EMBL; AF005046; AAD01210.1; -.
 DR EMBL; BC002921; AAH02921.1; -.
 DR EMBL; BC011368; AAH11368.1; -.
 DR EMBL; BC025282; AAH25282.1; -.
 DR HSSP; Q13153; 1F3M.
 DR GeneW; HGNC:16059; PAK4.
 DR H-InvDB; HIT0015110; -.
 DR MIM; 605451; -.
 DR GO; GO:0005794; C:Golgi apparatus; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000095; PAKbox/RhoGAP.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR011026; WASP_C.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR PROSITE; PS00107; S_TKC; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50010; PROTEIN_KINASE_DOM; 1.
 KW Alternative splicing; ATP-binding; Phosphorylation;
 KW Serine/threonine-protein kinase; Transferrase.
 FT DOMAIN 11
 FT DOMAIN 25
 FT NP_BIND 321 320 Linker.
 FT BINDING 327 335 Protein kinase.
 FT ACT_SITE 350 350 ATP (By similarity).
 FT VAAPSLIC 440 440 ATP (By similarity).
 FT 120 120 Proton acceptor (By similarity).
 FT 120 120 E -> K (in isoform 2).
 FT VARSPLIC 121 285 /Prid=VSP_004892.
 FT Missing (in isoform 2).
 SQ SEQUENCE 591 AA; 64071 MW; 04C2A5C0B06427D5 CRC64;

Query Match 96.5%; Score 436; DB 1; Length 591;
 Best Local Similarity 95.5%; Pred. No. 8.8e-36;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOQRRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVYHTRNNEE 60
 DB 356 KOQRRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVYHTRNNEE 60
 QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
 DB 416 QIAAVCLAVLQALAVLHAQGVHSDIKTD 444

RESULT 10
 ID 090M62 PRELIMINARY; PRT; 650 AA.
 AC 090M62;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE PAK5 protein.
 GN Name=PAK5.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stage VI oocyte;
 RA Cau J., Faure S., Delbert C., Morin N.;
 RL Submitted (May-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; A0277826; CAC40979.1; -
 DR HSSP; Q13153; 1F3M.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004661; P:protein amino acid phosphorylation; IEA.
 DR Pfam; PF00069; PBD; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding.
 SQ SEQUENCE 650 AA; 73736 MW; 9274DC6CADC4A081 CRC64;

Query Match 93.1%; Score 421; DB 2; Length 650;
 Best Local Similarity 89.9%; Pred. No. 3.2e-34;
 Matches 80; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOQRRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVYHTRNNEE 60
 DB 415 KOQRRELLFNEVYIMRDYRHEVNVEMNSYLVGDELWVMEFLGALTDIVYHTRNNEE 60
 QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
 DB 475 QIAAVCLAVLQALAVLHAQGVHSDIKTD 503

RESULT 11
 ID 06GM11 PRELIMINARY; PRT; 663 AA.
 AC 06GM11;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Zgc:92014.
 GN ORFNames=zgc:92014;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Uedtin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Grifwood J., Schmutz J., Bouffard G.G.,
 RA Rodriguez A.C., Grifwood J., Schmutz J., Myer R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Schnerker A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC074067; AAH74067.1; -
 DR ZFIN; ZDB-GENE-040704-69; zgc:92014.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011005; Kinase_lke.
 DR InterPro; IPR000095; PAKox/Rhodning.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_thr_kinase.
 DR InterPro; IPR011026; WASP_C.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KM ATP-binding.
 SQ SEQUENCE 663 AA; 74760 MW; 61F86F8876E40550 CRC64;
 Query Match 92.5%; Score 418; DB 2; Length 663;
 Best Local Similarity 89.9%; Pred. No. 6,7e-34;
 Matches 80; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDELMVYMEFLGGALTDIYHTMNEE 60
 |||||
 DB 428 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDELMVYMEFLGGALTDIYHTMNEE 487
 |||||

QY 61 QIAAVCLAVLQALAVLHAQGVISHDIKTD 89
 |||||
 DB 488 QISTVCLSVLKALSVLHSGGVIHRIKSD 516
 |||||

RESULT 12
 Q6NVJ4 PRELIMINARY; PRT; 711 AA.
 ID 06NVJ4;
 AC 06NVJ4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Hypochemical protein zgc:76890.
 GN ORFNames=zgc:76890;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derse J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smalins D.E., Schmech A., Schein J.E.,
 RA Jones S.J., Wray M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Strausberg R.;
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC068016; AAH68016.1;
 DR ZFIN, ZDB-GENE-040426-2085; zgc:76890.
 DR GO, GO:0005524; F-ATP binding; IEA.
 DR GO, GO:0004674; F-protein serine/threonine kinase activity; IEA.
 DR GO, GO:0004713; F-protein-tyrosine kinase activity; IEA.
 DR GO, GO:0006468; P-protein amino acid phosphorylation; IEA.
 DR InterPro, IPR011009; Kinase, like.
 DR InterPro, IPR000095; PAKbox/Rho-binding.
 DR InterPro, IPR000719; Prok. kinase.
 DR InterPro, IPR002290; Ser_Thr_kinase.
 DR InterPro, IPR001245; Tyr_kinase.
 DR InterPro, IPR011026; WASP_C.
 DR Pfam, PF00786; PBD; 1.
 DR Pfam, PF00069; Pkinase; 1.

DR Prodom; PD000001; Prok. Kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KM ATP-binding; Hypochemical protein.
 SQ SEQUENCE 711 AA; 78613 MW; D09E7B8D579D211B CRC64;
 Query Match 91.2%; Score 412; DB 2; Length 711;
 Best Local Similarity 88.8%; Pred. No. 2.9e-33;
 Matches 79; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDELMVYMEFLGGALTDIYHTMNEE 60
 |||||
 DB 476 KOORRELLFNEVYIMDHYHENVVEMVNSYLVGDELMVYMEFLGGALTDIYHTMNEE 535
 |||||

QY 61 QIAAVCLAVLQALAVLHAQGVISHDIKTD 89
 |||||
 DB 536 QIATVCLSVLKALSVLHSGGVIHRIKSD 564
 |||||

RESULT 13
 Q9CS71 PRELIMINARY; PRT; 229 AA.
 ID Q9CS71;
 AC Q9CS71;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched
 DE library, clone:573048107 product:SERINE/THREONINE-PROTEIN KINASE PAK
 DE 4 (EC 2.7.1.-) (P21-ACTIVATED KINASE 4) (PAK-4) homolog
 DE (fragment).
 GN Name=PAK4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RL "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA The PANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shiba K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multichipillary sequencer.",
 RL Genome Res. 10:11757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi U., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Akakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hasegaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koyama S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami T., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK017713; BAB30889.1; -
 DR HSSP; Q13153; 1P3M.
 DR MGD; MGI:1917834; Pak4.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_Kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KM Kinase.
 FT NON TER 1 1
 SQ SEQUENCE 229 AA; 25896 MW; D9CF2CA73CED941E CRC64;
 Query Match 90.5%; Score 409; DB 2; Length 229;
 Best Local Similarity 97.6%; Pred. No. 1.8e-33;
 Matches 80; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 8 LENEVYIMRDYRHNVENVWNSYLVGDELVMYMELEGALTDYITRRANEEOIAVCL 67
 DB 1 LFEVYIMDYRHNVENVWNSYLVGDELVMYMELEGALTDYITRRANEEOIAVCL 60
 QY 68 AVTQALAVYHAQGVYHSDIKTD 89
 DB 61 AVTQALAVYHAQGVYHSDIKTD 82
 RESULT 14
 Q8C015 PRELIMINARY; PRT; 719 AA.
 AC Q8C015
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
 DE enriched library, clone:6430627N20 Product:SERINE/THREONINE-PROTEIN
 DE KINASE PAK 5 (EC 2.7.1.-) (P21-ACTIVATED KINASE 5) (PAK-5)
 DE homolog.
 GN Name=PAK7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shiba K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multichipillary sequencer.",
 RL Genome Res. 10:11757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA Adachi U., Aizawa K., Akimura T., Akakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hayatsu N., Hiraoka T., Hiraoka T., Hori F.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohata N., Okazaki Y.,
 RA Saito R., Saito H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK032553; BAC27939.1; -
 DR HSSP; Q13153; 1P3M.
 DR MGD; MGI:1920334; Pak7.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006916; P:anti-apoptosis; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000095; PAKox/RhoGing.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR011026; WASP_C.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; s_Tkc; 1.

DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase.
 SQ SEQUENCE 719 AA; 80948 MW; 5E16D2318C238C8D CRC64;

Query Match 90.0%; Score 407; DB 2; Length 719;
 Best Local Similarity 87.6%; Pred. No. 9.5e-33;

Matches 78; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMEDYHENVEMVNSYLVGDELVMVEFLGALTDIVHTRMNEE 60
 DB 484 KOORRELLFNEVIMEDYHENVEMVNSYLVGDELVMVEFLGALTDIVHTRMNEE 543

QY 61 QIAVCLAVLQALAVLHAQGVISHDIKTD 89
 DB 544 QIATVCLSVLKALSYLHNOGVIRHDIKSD 572

RESULT 15

Q6RWS7 PRELIMINARY; PRT; 719 AA.
 AC Q6RWS7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE P21-activated kinase 5.
 GN Name=Pak7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=22879895; PubMed=14517284;
 RX DOI=10.1126/MCB.23.20.7134-7142.2003;
 RA Li X., Minden A.;
 RT "Targeted disruption of the gene for the PAK5 kinase in mice.";
 RL Mol. Cell. Biol. 23:7134-7142(2003).
 DR GO; GO:0005739; Cytochrome oxidase; IDA.
 DR GO; GO:0004674; F-protein serine/threonine kinase activity; IDA.
 DR GO; GO:0006916; P-anti-apoptosis; IDA.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000095; PAKbox/Rhodpding.
 DR InterPro; IPR002230; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR011026; WASP_C.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase.
 SQ SEQUENCE 719 AA; 80937 MW; 3A0159B9F14D34C7 CRC64;

Query Match 89.2%; Score 403; DB 2; Length 719;
 Best Local Similarity 86.5%; Pred. No. 2.4e-32;
 Matches 77; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMEDYHENVEMVNSYLVGDELVMVEFLGALTDIVHTRMNEE 60
 DB 484 KOORRELLFNEVIMEDYHENVEMVNSYLVGDELVMVEFLGALTDIVHTRMNEE 543

QY 61 QIAVCLAVLQALAVLHAQGVISHDIKTD 89
 DB 544 QIATVCLSVLKALSYLHNOGVIRHDIKSD 572

Search completed: March 15, 2005, 11:30:27
 Job time : 30.1029 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 10:56:56 ; Search time 30.6265 Seconds
(without alignment)
1123.919 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452
Sequence: 1 KQGRRELLFNEVIMRDYRH.....LQALVLAAGVYHSIDIKTD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.1Dec04:*

1: geneseqp1980a:*
2: geneseqp1990a:*
3: geneseqp2000a:*
4: geneseqp2001a:*
5: geneseqp2002a:*
6: geneseqp2003a:*
7: geneseqp2003bs:*
8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	100.0	89	AAV59139	AAV59139 Mouse ser
2	443	98.0	593	ADJ96654	Adj96654 Human bre
3	436	96.5	240	AAW93297	AAW93297 Human pol
4	436	96.5	240	ADC37303	ADC37303 Nuclear f
5	436	96.5	240	ADL30760	ADL30760 Human pro
6	436	96.5	250	AAV59129	AAV59129 Human PAK
7	436	96.5	293	ADL15851	ADL15851 PAK4KD pr
8	436	96.5	398	AAV55941	AAV55941 Human PAK
9	436	96.5	438	ADC37305	ADC37305 Nuclear f
10	436	96.5	501	ADC37309	ADC37309 Nuclear f
11	436	96.5	522	ABM84642	ABM84642 Human dia
12	436	96.5	522	ABM84644	ABM84644 Human dia
13	436	96.5	522	ABM84645	ABM84645 Human dia
14	436	96.5	588	ADH23359	ADH23359 Human p21
15	436	96.5	591	AAV55964	AAV55964 Human p21
16	436	96.5	591	AAV55918	AAV55918 Human ser
17	436	96.5	591	ADC37307	ADC37307 Nuclear f
18	436	96.5	591	ADH89973	ADH89973 Human can
19	436	96.5	591	ADP45079	ADP45079 Human kin
20	436	96.5	591	ADH23352	ADH23352 Human p21
21	436	96.5	591	ABM82101	ABM82101 Tumour-as
22	436	96.5	620	ABG19308	ABG19308 Novel hum
23	432	95.6	438	ADR39763	ADR39763 Human kin
24	416	92.0	338	ADL22704	ADL22704 Human dia
25	407	90.0	547	AA67825	AA67825 Human p21

26	407	90.0	719	4	AAAM38963	AAAM38963 Human pol
27	407	90.0	719	7	ADJ83007	Adj83007 Murine ma
28	402	88.9	457	8	ADH42207	Adh42207 Novel hum
29	402	88.9	457	8	ADH42215	Adh42215 Novel hum
30	402	88.9	457	8	ADH42211	Adh42211 Novel hum
31	402	88.9	457	8	ADH42217	Adh42217 Novel hum
32	402	88.9	457	8	ADH42213	Adh42213 Novel hum
33	402	88.9	580	7	ADW04603	Adw04603 Human pro
34	402	88.9	732	4	AAAB5788	AAAB5788 Human kin
35	402	88.9	719	4	AAAB5705	AAAB5705 Human pro
36	402	88.9	719	4	AAE02187	AAE02187 Human p21
37	402	88.9	719	7	ADC37451	ADC37451 Nuclear f
38	402	88.9	719	7	ADF45080	ADF45080 Human kin
39	402	88.9	719	7	ADJ83008	Adj83008 Human mam
40	402	88.9	719	8	ADJ29314	Adj29314 Human MAR
41	402	88.9	311	4	AAAB20336	AAAB20336 Human PAK
42	379	83.8	636	8	ADQ65328	ADQ65328 Novel hum
43	379	83.8	641	5	AAE16269	AAE16269 Human kin
44	379	83.8	681	2	AAV55940	AAV55940 Human PAK
45	379	83.8	681	3	AAAB03967	AAAB03967 Signal tr

ALIGNMENTS

RESULT 1	AAV59139	standard; protein, 89 AA.
ID	AAV59139	standard; protein, 89 AA.
XX	AAV59139;	
AC	XX	
XX	XX	
DT	08-MAR-2000	(first entry)
XX	XX	
DE	Mouse serine/threonine kinase, PAK4 partial protein sequence.	
XX	XX	
KW	PAK4; serine/threonine kinase; GRPase; intracellular signal cascade; Rac; Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; mouse; actin polymerization; filopodia; cancer; arthritis.	
XX	XX	
OS	Mus sp.	
PN	WO9963073-A1.	
XX	XX	
PD	09-DEC-1999.	
XX	XX	
PF	21-MAY-1999;	99WO-US011341.
XX	XX	
PR	21-MAY-1998;	98US-00082737.
XX	XX	
PA	(UYCO) UNIV COLUMBIA NEW YORK.	
XX	XX	
PI	Minden A;	
DR	WPI; 2000-072881/06.	
XX	XX	
PT	N-PSDB; AA240658.	
XX	XX	
PS	Novel mammalian nucleic acid useful for treating cancer and arthritis.	
XX	XX	
XX	Dislosure; Page 44; 95pp; English.	
CC	The invention relates to an isolated mammalian nucleic acid that encodes PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an effector for the GRPases Rac and Cdc42Hs which are involved in intracellular signal cascades, morphogenesis and mitogenesis, and activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of PAK4 with these enzymes will thus result in inhibition of actin polymerization and formation of filopodia. The PAK4 nucleic acid used for recombinant production of the protein, and as a source of probes for identifying homologous sequences and of (anti)sense oligonucleotides for inhibiting PAK4 expression. The protein, or its fragments, are used to raise specific antibodies and these are useful as ligands for therapeutic inhibition of interaction between PAK4 and its native binding partners. Inhibition of PAK4 activity or expression is used for treatment of cancer	

CC and arthritis. The present sequence represents the partial sequence of
CC mouse PAK4

XX Sequence 89 AA;

Query Match
Best Local Similarity 100.0%; Score 452; DB 3; Length 89;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQRRRELFNEVVIKRDYRHEVNVEMNSYLVGDELWVMEFLBGGALTDIVTHRMNEE 60

DB 1 KQRRRELFNEVVIKRDYRHEVNVEMNSYLVGDELWVMEFLBGGALTDIVTHRMNEE 60

QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89

DB 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89

RESULT 2
ADJ96654
ID ADJ96654 standard; protein; 593 AA.

AC ADJ96654;

DT 06-MAY-2004 (first entry)

DE Human sterile protein kinase STE20 Pak5_m protein SeqID 111.

XX Kinase; human; tyrosine protein kinase; serine/threonine protein kinase;

KM PK; STK; gene therapy; cancer; immune-related disease;

KM cardiovascular disease; brain; neuronal associated disease; metabolic;

KM inflammatory disorder; cytosolic; neuroprotective; immunomodulator;

XX antiinflammatory; enzyme; sterile protein kinase STE20; Pak5_m.

OS Homo sapiens.

OS 59.

PN WO2004006838-A2.

XX 22-JAN-2004.

PD 15-JUL-2003; 2003WO-US021730.

PR 15-JUL-2002; 2002US-0395632P.

XX (SUGEN-) SUGEN INC.

PI Whyte D, Manning G, Caenepeel S;

PT WPI; 2004-122753/12.

DR N-PSDB; ADJ96588.

XX New nucleic acid molecule encoding a kinase polypeptide, useful for

PT preparing a composition for treating diseases or disorders, e.g., cancer,

PT or neurological, immunological or inflammatory disorders.

XX Claim 1; SEQ ID NO 111; 366bp; English.

XX This invention relates to a novel isolated, enriched or purified nucleic

CC acid molecule that encodes a kinase polypeptide. Specifically, it relates

CC to human tyrosine and serine/threonine protein kinases (PK's and STK's),

CC as well as protein kinase-like enzymes. The present invention describes

CC screening methods to identify agonists, antagonists and antibodies that

CC can be used to modulate the activity or function of the mammalian kinase

CC enzymes. As such, these compositions can be used for gene therapy

CC purposes to treat diseases or disorders including cancer, immune-related

CC diseases, cardiovascular disease, brain or neuronal associated disease,

CC metabolic and inflammatory disorders. Accordingly, they exhibit

CC cytosolic, neuroprotective, immunomodulator and antiinflammatory

CC activities. This polypeptide sequence is a human kinase protein sequence

CC of the invention.

XX Sequence 593 AA;

Query Match
Best Local Similarity 98.0%; Score 443; DB 8; Length 593;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQRRRELFNEVVIKRDYRHEVNVEMNSYLVGDELWVMEFLBGGALTDIVTHRMNEE 60

DB 358 KQRRRELFNEVVIKRDYRHEVNVEMNSYLVGDELWVMEFLBGGALTDIVTHRMNEE 417

QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89

DB 418 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 446

RESULT 3
AAM93297
ID AAM93297 standard; protein; 240 AA.

AC AAM93297;

DT 06-NOV-2001 (first entry)

DE Human polypeptide, SEQ ID NO: 2793.

XX Human; full length cDNA; cDNA synthesis; oligo-capping.

OS Homo sapiens.

PN EP1130094-A2.

XX 05-SEP-2001.

PD 07-JUL-2000; 2000EP-00114089.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

PA Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

DR N-PSDB; AAK94217.

XX Claim 8; SEQ ID NO 2793; 1380bp + Sequence Listing; English.

PS The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been isolated

CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC been determined. Primers for synthesizing the full length cDNA are useful

CC for clarifying the function of the protein encoded by the cDNA. The full

CC length clones were obtained by construction of full length enriched cDNA

CC libraries that were synthesised by the oligo-capping method. The primers

CC enable the production of the full length cDNA easily without any special

CC methods. The present sequence is a polypeptide encoded by a full length

CC human cDNA of the invention. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in CD-ROM

CC format directly from EPO

XX Sequence 240 AA;

Query Match
Best Local Similarity 95.5%; Score 436; DB 4; Length 240;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQRRRELFNEVVIKRDYRHEVNVEMNSYLVGDELWVMEFLBGGALTDIVTHRMNEE 60

DB 5 KQRRRELFNEVVIKRDYRHEVNVEMNSYLVGDELWVMEFLBGGALTDIVTHRMNEE 64

QY 61 QIAAACLAVLQALAVLHAQGVTHSDIKTD 89
 DB 65 QIAAACLAVLQALSVLHAQGVTHSDIKSD 93

RESULT 4

ADCC37303
 ID ADC37303 standard; protein; 240 AA.

AC ADC37303;

DT 18-DEC-2003 (first entry)

DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 136.

KM Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 cancer; infectious disease; bone disease; AIDS;

KM neurodegenerative disease; ischemic disorder; Antiinflammatory;
 Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 Neuroprotective; Nootropic; Cardiant; Gene therapy; human.

OS Homo sapiens.

PN WO2003048202-A2.

PD 12-JUN-2003.

PF 03-DEC-2002; 2002WO-JP012644.

PR 03-DEC-2001; 2001JP-00366692.

PR 03-DEC-2001; 2001US-0335829P.

PR 03-OCT-2002; 2002JP-00291302.

PR 04-OCT-2002; 2002US-0415769P.

PA (ASAH) ASAHI KASEI KK.

PI Matsuda A, Muramatsu S;

DR WPI; 2003-505282/47.

DR N-PSDB; ADC37302.

PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 useful for treating inflammation, autoimmune diseases, cancers,
 infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 ischemic disorders.

PS Claim 1; SEQ ID NO 136; 938bp; English.

CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischemic disorders.

XX Sequence 240 AA;

Query Match 96.5%; Score 436; DB 7; Length 240;
 Best Local Similarity 95.5%; Pred. No. 5, 2e-48;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVVIMDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 60
 DB 5 KOORRELLFNEVVIMDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 64

QY 61 QIAAACLAVLQALAVLHAQGVTHSDIKTD 89
 DB 65 QIAAACLAVLQALSVLHAQGVTHSDIKSD 93

RESULT 5
 ADL30760

ID ADL30760 standard; protein; 240 AA.

AC ADL30760;

DT 20-MAY-2004 (first entry)

DE Human protein encoded by a full length cDNA clone segid 2793.

KM human; medicine; signal transduction; glycoprotein; transcription;
 KM oligo-capping method.

OS Homo sapiens.

PN EP1396543-A2.

PD 10-MAR-2004.

PF 07-JUL-2000; 2003EP-00025638.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00163865.

PR 07-JUL-2000; 2000EP-00114089.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Ota T, Nishikawa T, Isegaki T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2004-204755/20.

DR N-PSDB; ADL30759.

PT New oligonucleotide primers (830 CDNA) useful for synthesizing full
 PT length human CDNA.

PS Example 1; SEQ ID NO 2793; 1340bp; English.

CC This invention relates to a novel primers useful for synthesizing full
 CC length CDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This polypeptide sequence is a full
 CC length human protein of the invention.

XX Sequence 240 AA;

Query Match 96.5%; Score 436; DB 8; Length 240;
 Best Local Similarity 95.5%; Pred. No. 5, 2e-48;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVVIMDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 60
 DB 5 KOORRELLFNEVVIMDYRHENVEMVNSYLVGDELVMVMEFLGGALTDIVTHTMNEE 64

QY 61 QIAAACLAVLQALAVLHAQGVTHSDIKTD 89
 DB 65 QIAAACLAVLQALSVLHAQGVTHSDIKSD 93

RESULT 6
 AA59129
 ID AA59129 standard; protein; 250 AA.

AC AA59129;

DT 08-MAR-2000 (first entry)

DE Human PAK4 kinase domain fragment.

KM PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;

KW Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;
 KM actin polymerization; filopodia; cancer; arthritis; kinase domain.
 XX
 OS Homo sapiens.
 XX
 PN WO9963073-A1.
 XX
 PD 09-DEC-1999.
 XX
 PF 21-MAY-1999; 99WO-US011341.
 XX
 PR 21-MAY-1998; 98US-00082737.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Minden A;
 XX
 DR WPI; 2000-072881/06.
 XX
 PT Novel mammalian nucleic acid useful for treating cancer and arthritis.
 XX
 PS Disclosure; Fig 1c; 95pp; English.
 XX
 CC The invention relates to an isolated mammalian nucleic acid that encodes
 CC PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an
 CC effector for the GTPases Rac and Cdc42Hs which are involved in
 CC intracellular signal cascades, morphogenesis and mitogenesis, and
 CC activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of
 CC PAK4 with these enzymes will thus result in inhibition of actin
 CC polymerization and formation of filopodia. The PAK4 nucleic acid used for
 CC recombinant production of the protein, and as a source of probes for
 CC identifying homologous sequences and of (anti)sense oligonucleotides for
 CC inhibiting PAK4 expression. The protein, or its fragments, are used to
 CC raise specific antibodies and these are useful as ligands for therapeutic
 CC inhibition of interaction between PAK4 and its native binding partners.
 CC Inhibition of PAK4 activity or expression is used for treatment of cancer
 CC and arthritis. The present sequence represents the kinase domain fragment
 CC of human serine/threonine kinase, PAK4
 XX
 SQ Sequence 250 AA;

Query Match 96.5%; Score 436; DB 3; Length 250;
 Best Local Similarity 95.5%; Pred. No. 5.5e-48;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORELLFNEVIMRDYHENVEMVNSYLVGDELWVMEFLGALTDIVTHRMNEE 60
 DB 33 KQORELLFNEVIMRDYHENVEMVNSYLVGDELWVMEFLGALTDIVTHRMNEE 92
 QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89
 DB 93 QIAAVCLAVLQALVSLVHAQGVVHSDIKSD 121

RESULT 7
 ADE15851
 ID ADE15851 standard; protein; 293 AA.
 XX
 AC ADE15851;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE PAK4KD protein.
 XX
 KM PAK4KD protein.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087816-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 08-APR-2003; 2003WO-US010878.

XX
 PR 09-APR-2002; 2002US-0371018P.
 PR 02-DEC-2002; 2002US-0430567P.
 XX
 XX (STRU-) STRUCTURAL GENOMIX INC.
 XX
 PI Antonyam SS, Fell I, Buchanan SG, Post KW, Liu Y, Lorber D;
 XX
 DR WPI; 2003-853974/79.
 XX
 PT Producing a computer-readable database comprising the three-dimensional
 PT molecular structural coordinates of a binding pocket of a PAK4D protein,
 PT comprises introducing the structural coordinates into a computer.
 XX
 PS Claim 17; SEQ ID NO 5; 421pp; English.
 XX
 CC The present invention relates to producing a computer-readable database
 CC comprising the three-dimensional molecular structural coordinates of a
 CC binding pocket of a PAK4D protein, comprising introducing the structural
 CC coordinates to into a computer to produce a database containing the
 CC molecular structural coordinates of the protein or binding pocket. The
 CC method is useful for producing a machine-readable database for
 CC identifying and designing inhibitors, activators and mutants of PAK4D,
 CC PAK4D crystals and compounds or compositions that affect PAK4D
 CC activity. The present sequence represents a primer of the invention.
 XX
 SQ Sequence 293 AA;

Query Match 96.5%; Score 436; DB 7; Length 293;
 Best Local Similarity 95.5%; Pred. No. 6.9e-48;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQORELLFNEVIMRDYHENVEMVNSYLVGDELWVMEFLGALTDIVTHRMNEE 60
 DB 58 KQORELLFNEVIMRDYHENVEMVNSYLVGDELWVMEFLGALTDIVTHRMNEE 117
 QY 61 QIAAVCLAVLQALAVLHAQGVVHSDIKTD 89
 DB 118 QIAAVCLAVLQALVSLVHAQGVVHSDIKSD 146

RESULT 8
 AAY55941
 ID AAY55941 standard; protein; 398 AA.
 XX
 AC AAY55941;
 XX
 DT 18-FEB-2000 (first entry)
 XX
 DE Human PAK5 protein.
 XX
 KM Antithrombotic; antithrombotic; antiinflammatory; antiallergic; osteopathic;
 KM antiproliferative; antiarteriosclerotic; antiaesthetic; immunosuppressive;
 KM neuroprotective; cardiac; cerebroprotective; cytoprotective; antidiabetic;
 KM vulnery; STE20; protein kinase; STK3; STK3; STK4; STK5; STK6; STK7;
 KM ZC1; ZC2; ZC3; ZC4; KH2; SUU1; SUU3; GEK3; PAK4; PAK5; antagonist;
 KM antibody; gene therapy; rheumatoid arthritis; arteriosclerosis; asthma;
 KM inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
 KM rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
 KM myocardial infarction; cardiovascular disease; stroke; renal failure;
 KM oxidative stress-related neurodegenerative disorder; Parkinson's disease;
 KM amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
 KM ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
 KM meangial disorder; growth regulation; wound healing; T cell activation;
 KM immunosuppressant.
 XX
 OS Homo sapiens.
 XX
 PN WO9953036-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008150.

XX	PR	14-APR-1998;	98US-0081784P.	
XX	XX	(SUGEN-)	SUGEN INC.	
XX	PI	Plowman G, Martinez R, Whyte D;		
XX	DR	WPI; 1999-611301/52.		
XX	DR	N-PSDB; AAZ40493.		
XX	PT	Novel kinase-related polypeptides used for the diagnosis and treatment of		
XX	PT	kinase-related diseases and disorders.		
XX	PS	Disclosure; Page 310-312; 387pb; English.		
XX	XX			
CC	CC	This sequence represents a novel STE20-related protein kinase. The		
CC	CC	invention relates to nucleic acid molecule encoding a kinase polypeptide		
CC	CC	selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,		
CC	CC	ZC4, KMS2, STU01, STU03, GEX3, PAK4 and PAK5. The proteins are used to		
CC	CC	identify agonists and antagonists, and to raise antibodies. The		
CC	CC	polynucleotides are useful in gene therapy protocols. The polynucleotides,		
CC	CC	polypeptides, antibodies, antagonists and agonists may be used to treat		
CC	CC	diseases such as immune-related disorders and diseases (e.g. rheumatoid		
CC	CC	arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.		
CC	CC	Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,		
CC	CC	rheinitis, autoimmunity, and organ transplantation, chronic inflammatory		
CC	CC	pelvic disease, multiple sclerosis, organ transplantation, myocardial		
CC	CC	infarction, cardiovascular disease, stroke, renal failure, oxidative		
CC	CC	stress-related neurodegenerative disorders (e.g. amyotrophic lateral		
CC	CC	sclerosis, Parkinson's disease and Leigh syndrome), cancer,		
CC	CC	cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes		
CC	CC	mellitus, fibrotic and mesangial disorders. The proteins may also be		
CC	CC	useful for cell growth regulation (e.g. in wound healing), T cell		
CC	CC	activation, mitosis control, and as immunosuppressants		
XX	XX			
SQ	SQ	Sequence 398 AA;		
		Query Match 96.5%; Score 436; DB 2; Length 398;		
		Best Local Similarity 95.5%; Pred. No. 1, 1e-47;		
		Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0		
Oy		1 KOQRELLFENEVIVIRDYRHEWVEMVNSYLVGDELVMVMEFLGGALTDIVYHTRMNE 60		
Db		163 KOQRELLFENEVIVIRDYRHEWVEMVNSYLVGDELVMVMEFLGGALTDIVYHTRMNE 222		
Oy		61 QIAAVCLAVTQALAVLAAGVTHSDIKTD 89		
Db		223 QIAAVCLAVTQALAVLAAGVTHSDIKSD 251		
		RESULT 9		
		ADC37305		
XX	XX	ADC37305 standard; protein; 438 AA.		
XX	XX	ADC37305;		
XX	DT	18-DEC-2003 (first entry)		
XX	DE	Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 139.		
XX	XX			
KW	KW	Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;		
KW	KW	cancer; infectious disease; bone disease; AIDS;		
KW	KW	neurodegenerative disease; ischaemic disorder; Antiinflammatory;		
KW	KW	immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;		
XX	XX	Neuroprotective; Nootropic; Cardiac; Gene therapy; human.		
XX	OS	Homo sapiens.		
XX	PN	WO2003048202-A2.		
XX	PD	12-JUN-2003.		
XX	XX			
PF	XX	03-DEC-2002; 2002WO-JP012644.		

XX	03-DEC-2001; 2001JP-00368692.
PR	05-DEC-2001; 2001US-0335829P.
PR	03-OCT-2002; 2002JP-00291302.
PR	04-OCT-2002; 2002US-0415769P.
XX	
PA	(ASAH) ASAH KASEI KK.
XX	
PI	Matsuda A, Muramatsu S;
XX	
DR	WPI; 2003-505282/47.
DR	N-PSDB; ADC37304.
XX	
PT	New purified protein that activates nuclear factor kappa B (NF-kappaB) ,
PT	useful for treating inflammation, autoimmune diseases, cancers,
PT	infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT	ischemic disorders.
XX	
PS	Claim 1; SEQ ID NO 138; 938pp; English.
XX	
CC	The present invention relates to novel proteins and their coding
CC	sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC	kappaB). The proteins and their coding sequences are useful for treating
CC	a disease associated with NF-kappaB activation, such as inflammation,
CC	autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC	neurodegenerative diseases, or ischemic disorders.
XX	
SQ	Sequence 438 AA;
XX	
Query Match	96.5%; Score 436; DB 7; Length 438;
Best Local Similarity	95.5%; Pred. No. 1.2e-47;
Matches	85; Conservative 3; Mismatches 1; Indels 0; Gaps 0
QY	1 KQQRRELLFNEVIMRDYRHNVENVMNSYLVGDELVMMEFLGALTDIVYHTRNNE 60
DB	203 KQQRRELLFNEVIMRDYRHNVENVMNSYLVGDELVMMEFLGALTDIVYHTRNNE 262
QY	61 QIAVCLAVLQALVLAHQSYTHSDIKTD 89
DB	263 QIAVCLAVLQALSVLAHQGYIHRDIKSD 291
RESULT 10	
ID	ADC37309 standard; protein, 501 AA.
AC	ADC37309;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 142.
XX	
KW	Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW	cancer; infectious disease; bone disease; AIDS;
KW	neurodegenerative disease; ischaemic disorder; Antiinflammatory;
KW	immunomodulator; Cytostratic; Antimicrobial; Osteopethic; Anti-HIV;
KW	Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
XX	
OS	Homo sapiens.
XX	
PN	WO2003048202-A2.
XX	
PD	12-JUN-2003.
XX	
PP	03-DEC-2002; 2002WO-JP012644.
XX	
PR	03-DEC-2001; 2001JP-00368692.
PR	05-DEC-2001; 2001US-0335829P.
PR	03-OCT-2002; 2002JP-00291302.
PR	04-OCT-2002; 2002US-0415769P.
XX	
PA	(ASAH) ASAH KASEI KK.
XX	

PI Mateuda A, Muramatsu S;
XX
DR WPI; 2003-505282/47.
XX N-PSDB; AOC37308.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
PS Claim 1; SEQ ID NO 142; 938bp; English.
XX
CC The present invention relates to novel proteins and their coding
CC sequences (ADCC37168-ADCC37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischemic disorders.
XX
SQ Sequence 501 AA;
XX
Query Match 96.5%; Score 436; DB 7; Length 501;
Best Local Similarity 95.5%; Pred. No. 1.5e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOORRELLFNEVYIMRDYRHHENYVEMNSYLVGDELWVMEFLGALTDIYTHRMNEE 60
DB 266 KOORRELLFNEVYIMRDYRHHENYVEMNSYLVGDELWVMEFLGALTDIYTHRMNEE 60
QY 61 QIAAVCLAVLQALSVLHAQGVYHSDIKTD 89
DB 326 QIAAVCLAVLQALSVLHAQGVYHSDIKSD 354
XX
RESULT 11
ABM84642
ID ABM84642 standard; protein; 522 AA.
XX
AC ABM84642;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic protein SEQ ID NO:4891.
XX
KM Gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorn TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV,
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI Peralta CH, Anderson SB, Rlouk P, Shen EJ, Wu MC, Stuve IL,
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES,
PI Xu Y, Kwong M, Policky JU, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN43294.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC infection, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm
XX
SQ Sequence 522 AA;
XX
Query Match 96.5%; Score 436; DB 8; Length 522;
Best Local Similarity 95.5%; Pred. No. 1.5e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOORRELLFNEVYIMRDYRHHENYVEMNSYLVGDELWVMEFLGALTDIYTHRMNEE 60
DB 287 KOORRELLFNEVYIMRDYRHHENYVEMNSYLVGDELWVMEFLGALTDIYTHRMNEE 346
QY 61 QIAAVCLAVLQALSVLHAQGVYHSDIKTD 89
DB 347 QIAAVCLAVLQALSVLHAQGVYHSDIKSD 375
XX
RESULT 12
ABM84644
ID ABM84644 standard; protein; 522 AA.
XX
AC ABM84644;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic protein SEQ ID NO:4893.
XX
KM Gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorn TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV,
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI Peralta CH, Anderson SB, Rlouk P, Shen EJ, Wu MC, Stuve IL,
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES,
PI Xu Y, Kwong M, Policky JU, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN43296.
XX

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm

XX Sequence 522 AA;
 SQ

Query Match 96.5%; Score 436; DB 8; Length 522;
 Best Local Similarity 95.5%; Pred. No. 1.5e-47;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVYTHRMNEE 60
 DB 287 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVYTHRMNEE 346
 OY 61 QIAAVCLAVLQALSVLHAQGVIRHDIKTD 89
 DB 347 QIAAVCLAVLQALSVLHAQGVIRHDIKSD 375

RESULT 13
 ABM84645
 ID ABM84645 standard; protein; 522 AA.
 AC ABM84645;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4894.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harshbome TA, Suchorski MT, Altus CM, Plets SJ, Bider LV;
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilett UA, Kliron BS;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletsen D;
 PI Patuary S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.
 DR N-PSDB; ACN43297.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm

XX Sequence 522 AA;
 SQ

Query Match 96.5%; Score 436; DB 8; Length 522;
 Best Local Similarity 95.5%; Pred. No. 1.5e-47;
 Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVYTHRMNEE 60
 DB 287 KOORRELLFNEVIMRDYHENVVEMVNSYLVGDELMVMEFLGGALTDIVYTHRMNEE 346
 OY 61 QIAAVCLAVLQALSVLHAQGVIRHDIKTD 89
 DB 347 QIAAVCLAVLQALSVLHAQGVIRHDIKSD 375

RESULT 14
 ADH23359
 ID ADH23359 standard; protein; 588 AA.
 AC ADH23359;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human p21 (CDKN1A)-activated kinase 4 (PAK4) serine/threonine kinase #1.
 XX
 KW human; p21 (CDKN1A)-activated kinase 4; PAK4; serine/threonine kinase;
 KW enzyme; HIV-Tat transcriptional activity.
 XX
 OS Homo sapiens.
 XX
 PN US2003186254-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 29-APR-2002; 2002US-00134102.
 XX
 PR 30-DEC-1999; 99US-0173939P.
 PR 28-DEC-2000; 2000US-00750457.
 XX
 PA (CELL-) CELL SIGNALING TECHNOLOGY INC.
 PI Melnick MB, Moritz A, Comb MJ;
 PI WPI; 2004-130707/13.
 DR N-PSDB; ADH23361.

XX New isolated DNA sequence encoding PAK4 serine/threonine kinase for
PT modulating the transcriptional activity of human immunodeficiency virus-
PT Tat protein.

PS Claim 1; SEQ ID NO 1; 47bp; English.

CC The invention relates to an isolated DNA sequence encoding p21 (CDKN1A) -
CC activated kinase 4 (PAK4) serine/threonine kinase. The invention is
CC useful for modulating the transcriptional activity of HIV-Tat protein.
CC The invention provides isolated DNA and vectors encoding PAK4 and Cdc42-
CC GEF which synergize to stimulate Tat transcriptional activity. The
CC present sequence represents the amino acid sequence of human PAK4.
XX

SO Sequence 588 AA;

Query Match 96.5%; Score 436; DB 8; Length 588;
Best Local Similarity 95.5%; Pred. No. 1.8e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQORRELLFNEVYIMRDYHENVVEMVNSYLVGDELWVMEFLGGALTDIVTHTRNNEE 60

DB 356 KQORRELLFNEVYIMRDYHENVVEMVNSYLVGDELWVMEFLGGALTDIVTHTRNNEE 415

OY 61 QIAAVCLAVLQALAVLHAGVTHSDIKTD 89

DB 416 QIAAVCLAVLQALAVLHAGVTHSDIKTD 444

RESULT 15

AAVS5964
ID AAVS5964 standard; protein; 591 AA.

AC AAVS5964;

DT 18-FEB-2000 (first entry)

DE Full length human PAK5 protein.

KM Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;
KM antiporiatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;
KM neuroprotective; cardiac; cerebroprotective; cytostatic; antidiabetic;
KM vulnerability; STK20; protein kinase; STK2; STK3; STK4; STK5; STK6; STK7;
KM ZC1; ZC2; ZC3; ZC4; KHS2; STU1; STU3; GSK2; PAK4; PAK5; antagonist;
KM antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;
KM inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KM rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KM myocardial infarction; cardiovascular disease; stroke; renal failure;
KM oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KM amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KM ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KM mesangial disorder; growth regulation; wound healing; T cell activation;
KM immunosuppressant.

OS Homo sapiens.

XX WO953036-A2.

XX 21-OCT-1999.

XX 13-APR-1999; 99WO-US008150.

XX 14-APR-1998; 98US-0081784P.

XX (SUGEN) SUGEN INC.

XX Plowman G, Martinez R, Whyte D;

XX WPI; 1999-611301/52.

XX N-PSDB; AA240538.

XX Novel kinase-related polypeptides used for the diagnosis and treatment of
PT kinase-related diseases and disorders.

XX Claim 11; Page 366-368; 387pp; English.

CC This sequence represents a novel STK20-related protein kinase. The
CC invention relates to nucleic acid molecule encoding a kinase polypeptide
CC selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3,
CC ZC4, KHS2, STU1, STU3, GSK2, PAK4 and PAK5. The proteins are used to
CC identify agonists and antagonists, and to raise antibodies. The
CC polynucleotides are useful in gene therapy protocols. The polynucleotides,
CC polypeptides, antibodies, antagonists and agonists may be used to treat
CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC disease, multiple sclerosis, organ transplantation, myocardial
CC infarction, cardiovascular disease, stroke, renal failure, oxidative
CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC mellitus, fibrotic and mesangial disorders. The proteins may also be
CC useful for cell growth regulation (e.g. in wound healing), T cell
CC activation, mitosis control, and as immunosuppressants

SO Sequence 591 AA;

Query Match 96.5%; Score 436; DB 2; Length 591;
Best Local Similarity 95.5%; Pred. No. 1.8e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KQORRELLFNEVYIMRDYHENVVEMVNSYLVGDELWVMEFLGGALTDIVTHTRNNEE 60

DB 356 KQORRELLFNEVYIMRDYHENVVEMVNSYLVGDELWVMEFLGGALTDIVTHTRNNEE 415

OY 61 QIAAVCLAVLQALAVLHAGVTHSDIKTD 89

DB 416 QIAAVCLAVLQALAVLHAGVTHSDIKTD 444

Search completed: March 15, 2005, 11:26:31
Job time : 31.6265 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 11:30:37 ; Search time 24.2132 Seconds

(without alignments)
1212.403 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452
Sequence: 1 KQORRELFNEVIMRDYRH.....LQALAVLAAGVTHSDIKTD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	100.0	89	US-10-693-367-14	Sequence 14, Appl
2	443	98.0	292	US-10-406-676-7	Sequence 7, Appl
3	443	98.0	292	US-10-406-676-12	Sequence 12, Appl
4	443	98.0	593	US-10-618-941-11	Sequence 11, Appl
5	436	96.5	250	US-10-693-367-3	Sequence 3, Appl
6	436	96.5	292	US-10-406-676-5	Sequence 5, Appl
7	436	96.5	292	US-10-406-676-6	Sequence 6, Appl
8	436	96.5	292	US-10-406-676-8	Sequence 8, Appl
9	436	96.5	292	US-10-406-676-9	Sequence 9, Appl
10	436	96.5	292	US-10-406-676-10	Sequence 10, Appl
11	436	96.5	292	US-10-406-676-11	Sequence 11, Appl
12	436	96.5	293	US-10-406-676-4	Sequence 4, Appl
13	436	96.5	398	US-09-291-417-30	Sequence 30, Appl

14	436	96.5	588	US-10-134-102-1	Sequence 1, Appl
15	436	96.5	591	US-09-291-417-103	Sequence 103, Appl
16	436	96.5	591	US-10-134-102-4	Sequence 4, Appl
17	436	96.5	591	US-10-394-322A-48	Sequence 48, Appl
18	436	96.5	591	US-10-693-367-2	Sequence 2, Appl
19	436	96.5	591	US-10-893-025-5	Sequence 5, Appl
20	421	93.1	292	US-10-406-676-15	Sequence 15, Appl
21	407	90.0	290	US-10-406-676-13	Sequence 13, Appl
22	407	90.0	719	US-10-331-095-2	Sequence 2, Appl
23	402	88.9	290	US-10-406-676-14	Sequence 14, Appl
24	402	88.9	290	US-10-406-676-16	Sequence 16, Appl
25	402	88.9	290	US-10-406-676-17	Sequence 17, Appl
26	402	88.9	580	US-10-108-260A-3288	Sequence 3288, Appl
27	402	88.9	719	US-10-331-095-4	Sequence 4, Appl
28	402	88.9	719	US-10-394-322A-49	Sequence 49, Appl
29	379	83.8	292	US-10-406-676-21	Sequence 21, Appl
30	379	83.8	641	US-10-311-034-15	Sequence 15, Appl
31	379	83.8	681	US-09-291-417-29	Sequence 29, Appl
32	376	83.2	681	US-09-765-815-2	Sequence 2, Appl
33	366	81.0	290	US-10-406-676-18	Sequence 18, Appl
34	366	81.0	290	US-10-406-676-19	Sequence 19, Appl
35	366	81.0	290	US-10-406-676-20	Sequence 20, Appl
36	366	81.0	635	US-10-134-102-2	Sequence 2, Appl
37	366	81.0	639	US-10-134-102-6	Sequence 6, Appl
38	303	67.0	542	US-10-369-493-6482	Sequence 6482, Appl
39	303	67.0	542	US-10-369-493-6483	Sequence 6483, Appl
40	283	62.6	704	US-10-267-502-378	Sequence 378, Appl
41	277	61.3	297	US-10-664-421-34	Sequence 34, Appl
42	277	61.3	305	US-09-765-815-10	Sequence 10, Appl
43	277	61.3	305	US-10-664-421-48	Sequence 48, Appl
44	277	61.3	545	US-09-967-624-5	Sequence 5, Appl
45	277	61.3	545	US-10-394-322A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-10-693-367-14
Sequence 14, Application US/10693367
Publication No. US20040091992A1
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: Minden, Audrey
TITLE OF INVENTION: PAR4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
FILE REFERENCE: 575/55311-A-PCT-US
CURRENT FILING DATE: 2003-10-24
PRIORITY FILING DATE: 2003-10-24
PRIORITY FILING DATE: 2000-11-21
PRIORITY FILING DATE: 1999-05-21
PRIORITY FILING DATE: 1999-05-21
PRIORITY FILING DATE: 1998-05-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 89
TYPE: PRT
ORGANISM: mouse
US-10-693-367-14

Query Match 100.0%; Score 452; DB 15; Length 89;
Best Local Similarity 100.0%; Pred. No. 1e-41;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYRHENNYNSYLVGDELAVMVEFLGALTDIVTHRMNE 60
DB 1 KQORRELFNEVIMRDYRHENNYNSYLVGDELAVMVEFLGALTDIVTHRMNE 60
QY 61 QIAAVCLAVLQALAVLAAGVTHSDIKTD 89
DB 61 QIAAVCLAVLQALAVLAAGVTHSDIKTD 89

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RESULT 2
US-10-406-676-7
; Sequence 7, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 292
; TYPE: PRT
; ORGANISM: M.musculus
US-10-406-676-7

Query Match          98.0%; Score 443; DB 15; Length 292;
Best Local Similarity 97.8%; Pred. No. 3.8e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYRHENVEMVNSYLVGDELMVMEFLGGLTDTIVTTRMNEE 60
DB 57 KQQRRELLFNEVIMRDYRHENVEMVNSYLVGDELMVMEFLGGLTDTIVTTRMNEE 116
DB 117 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 145

RESULT 3
US-10-406-676-12
; Sequence 12, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Anthonyamy, Stephen
; APPLICANT: Feil, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 292
; TYPE: PRT
; ORGANISM: M.musculus
US-10-406-676-12
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Query Match          98.0%; Score 443; DB 15; Length 292;
Best Local Similarity 97.8%; Pred. No. 3.8e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYRHENVEMVNSYLVGDELMVMEFLGGLTDTIVTTRMNEE 60
DB 57 KQQRRELLFNEVIMRDYRHENVEMVNSYLVGDELMVMEFLGGLTDTIVTTRMNEE 116
DB 117 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 145

RESULT 4
US-10-618-941-111
; Sequence 111, Application US/10618941
; Publication No. US2004019792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERRARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-618-941-111

Query Match          98.0%; Score 443; DB 16; Length 593;
Best Local Similarity 97.8%; Pred. No. 8.5e-40;
Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQQRRELLFNEVIMRDYRHENVEMVNSYLVGDELMVMEFLGGLTDTIVTTRMNEE 60
DB 358 KQQRRELLFNEVIMRDYRHENVEMVNSYLVGDELMVMEFLGGLTDTIVTTRMNEE 417
DB 418 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 446

RESULT 5
US-10-693-367-3
; Sequence 3, Application US/10693367
; Publication No. US20040091992A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/693,367
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US/09/718,032
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: human
US-10-693-367-3
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Best Local Similarity 95.5%; Pred. No. 1.8e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 33 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 92
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 93 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 121
    |||||

RESULT 6
US-10-406-676-5
; Sequence 5, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-5

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 57 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 116
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 117 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 145
    |||||

RESULT 7
US-10-406-676-6
; Sequence 6, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-6
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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-676-6

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 57 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 116
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 117 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 145
    |||||

RESULT 9
US-10-406-676-9
; Sequence 9, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-406-676-8

Query Match          96.5%; Score 436; DB 15; Length 292;
Best Local Similarity 95.5%; Pred. No. 2.2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 60
    |||||
DB 57 KOORRELLFNEVIMRDYHENVEMVNSYLVGDELMVMEFLGALTDIVTHTRMNEE 116
    |||||

QY 61 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 89
    |||||
DB 117 QIAAVCLAVLQALSVLHAQGVTHSDIKTD 145
    |||||

RESULT 8
US-10-406-676-8
; Sequence 8, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonyasamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lorber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-406-676-8
```

```

1  APPLICANT: Fell, Ingeborg
2  APPLICANT: Buchanan, Sean
3  APPLICANT: Post, Kai W.
4  APPLICANT: Liu, Yi
5  APPLICANT: Lober, David
6  TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4D KINASE
7  TITLE OF INVENTION: PAK4D
8  FILE REFERENCE: 524982002300
9  CURRENT APPLICATION NUMBER: US/10/406,676
10 CURRENT FILING DATE: 2003-04-02
11 PRIOR APPLICATION NUMBER: 60/371,018
12 PRIOR FILING DATE: 2002-04-09
13 PRIOR APPLICATION NUMBER: 60/430,567
14 PRIOR FILING DATE: 2002-12-02
15 NUMBER OF SEQ ID NOS: 21
16 SOFTWARE: FastSeq for Windows Version 4.0
17 SEQ ID NO 9
18 LENGTH: 292
19 TYPE: PRT
20 ORGANISM: H.sapiens
21 US-10-406-676-9

```

	Query Match	Similarity	Score	DB	Length
Best Local	85	95.5%	436	15	292
Matches	85	Conservative	3	Mismatches	1
				Indels	0
				Gaps	0
QY	1	KQQRRELLFENVYIMRDYRHEENVEMNYSYLGDGLAVMVEFLGALTDITYTRNME	60		
Db	57	KQQRRELLFENVYIMRDYRHEENVEMNYSYLGDGLAVMVEFLGALTDITYTRNME	116		
QY	61	QIAAVGLAVLQALAVLHAQGVYIHSDDIKTD	89		
Db	117	QIAAVGLAVLQALAVLHAQGVYIHRDIKSD	145		

```

RESULT 10
US-10-406-676-10
; Sequence 10, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lotber, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; TITLE OF INVENTION: PAK4KD
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
; US-10-406-676-10

```

Query Match	96.5%	Score 436;	DB 15;	Length 292;
Best Local Similarity	95.5%	Pred. No. 2.2e-39;		
Matches	85;	Conservative 3;	Mismatches 1;	Indels 0; Gaps 0;
OY	1	KQQRRELLFENVITMRDYYRHENVVEMVNSYLVGBELVWMEFLFGALGALTDIVYTHRNME	60	
Db	57	KQQRRELLFENVITMRDYYRHENVVEMVNSYLVGBELVWMEFLFGALGALTDIVYTHRNME	116	
OY	61	QIAAVCLAVICALLAVILHAGQVITHSDIKTD	89	

```

Db      117 QIAAVCLAVLQALSVLHAQGVTHRDIKSD 145
          |||||:|||||:|

```

```

RESULT 11
US-10-406-676-11
; Sequence 11, Application US/10406676
; Publication No. US20030229453A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: AntonySamy, Stephen
; APPLICANT: Fell, Ingeborg
; APPLICANT: Buchanan, Sean
; APPLICANT: Post, Kai W.
; APPLICANT: Liu, Yi
; APPLICANT: Lotbet, David
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
; TITLE OF INVENTION: PAK4KD
; FILE REFERENCE: 524982002300
; CURRENT APPLICATION NUMBER: US/10/406,676
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/371,018
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/430,567
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 292
; TYPE: PRT
; ORGANISM: H.sapiens
US-10-406-676-11

```

Query Match	96.5%;	Score 436;	DB 15;	Length 292;
Best Local Similarity	95.5%;	Pred. No. 2, 2e-33;		
Matches	85;	Conservative	3;	Mismatches 1;
			Indels	0;
			Gaps	0;
QY	1	KQQRRELLFNEBVIMRDYRHENTVVENMNSYLVDGLVWVMEFLLEGALTDIVTHTRNNEE	60	
Db	57	KQQRRELLFNEBVIMRDYRHENTVVENMNSYLVDGLVWVMEFLLEGALTDIVTHTRNNEE	116	
QY	61	QIAAVCLAVLQALAVLHAQGVIHSDIKTD	89	
Db	117	QIAAVCLAVLQALSVLHAQGVIHSDIKSD	145	

```

RESULT 12
US-10-406-676-4
: Sequence 4, Application US/10406676
: Publication No. US20030229453A1
: GENERAL INFORMATION:
: APPLICANT: Structural Genomix, Inc.
: APPLICANT: Antonysamy, Stephen
: APPLICANT: Fell, Ingeborg
: APPLICANT: Buchanan, Sean
: APPLICANT: Post, Kai W.
: APPLICANT: Liu, Yi
: APPLICANT: Iober, David
: TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
: TITLE OF INVENTION: PAK4KD
: FILE REFERENCE: 524982002300
: CURRENT APPLICATION NUMBER: US/10/406,676
: CURRENT FILING DATE: 2003-04-02
: PRIOR APPLICATION NUMBER: 60/371,018
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/430,567
: PRIOR FILING DATE: 2002-12-02
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 293
: TYPE: PRT
: ORGANISM: Homo sapiens

```

US-10-406-676-4

Query Match 96.5%; Score 436; DB 15; Length 293;
Best Local Similarity 95.5%; Pred. No. 2,2e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFNEVYIMRDYHENVNEMNSYLVGDELMVMEFLGGALTDIVHTRMNEE 60
DB 58 KOORRELFNEVYIMRDYHENVNEMNSYLVGDELMVMEFLGGALTDIVHTRMNEE 117

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 118 QIAAVCLAVLQALSVLHAQGVHSDIKSD 146

RESULT 13

US-09-291-417-30
Sequence 30, Application US/09291417A
Publication No. US20030050230A1

GENERAL INFORMATION:
APPLICANT: PLOMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 240/300

CURRENT APPLICATION NUMBER: US/09/291,417A

CURRENT FILING DATE: 1999-04-13

EARLIER APPLICATION NUMBER: US 60/081,784

EARLIER FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 147

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 30

LENGTH: 398

TYPE: PRT

ORGANISM: Mammalian (Human) PAK5

US-09-291-417-30

Query Match 96.5%; Score 436; DB 10; Length 398;
Best Local Similarity 95.5%; Pred. No. 3.1e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 14

US-10-134-102-1
Sequence 1, Application US/10134102
Publication No. US20030186254A1

GENERAL INFORMATION:
APPLICANT: Melnick, Michael B.
APPLICANT: Moritz, Albrecht
TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
FILE REFERENCE: CST-176 CIP
CURRENT APPLICATION NUMBER: US/10/134,102
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: 09/750,457
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/173,939
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 588
TYPE: PRT
ORGANISM: Homo sapiens

US-10-134-102-1

Query Match 96.5%; Score 436; DB 14; Length 588;
Best Local Similarity 95.5%; Pred. No. 4.9e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFNEVYIMRDYHENVNEMNSYLVGDELMVMEFLGGALTDIVHTRMNEE 60
DB 356 KOORRELFNEVYIMRDYHENVNEMNSYLVGDELMVMEFLGGALTDIVHTRMNEE 415

QY 61 QIAAVCLAVLQALAVLHAQGVHSDIKTD 89
DB 416 QIAAVCLAVLQALSVLHAQGVHSDIKSD 444

RESULT 15

US-09-291-417-103
Sequence 103, Application US/09291417A
Publication No. US20030050230A1

GENERAL INFORMATION:
APPLICANT: PLOMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 240/300

CURRENT APPLICATION NUMBER: US/09/291,417A

CURRENT FILING DATE: 1999-04-13

EARLIER APPLICATION NUMBER: US 60/081,784

EARLIER FILING DATE: 1998-04-14

NUMBER OF SEQ ID NOS: 147

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 103

LENGTH: 591

TYPE: PRT

ORGANISM: Full length Mammalian (Human) PAK5hu

US-09-291-417-103

Query Match 96.5%; Score 436; DB 10; Length 591;
Best Local Similarity 95.5%; Pred. No. 4.9e-39;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Search completed: March 15, 2005, 11:48:06
Job time : 32.2132 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 15, 2005, 11:18:02 ; Search time 7.85294 Seconds

(without alignments)
846.023 Million cell updates/sec

Title: US-10-693-367-14

Perfect score: 452
Sequence: 1 KQORRELFNEVIMRDYH.....LQALAVLHAQVTHSDIKTD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	452	100.0	89	4	US-09-718-032-14	Sequence 14, Appl
2	436	96.5	250	3	US-09-082-737-3	Sequence 3, Appl
3	436	96.5	250	4	US-09-718-032-3	Sequence 3, Appl
4	436	96.5	398	4	US-09-688-1888-30	Sequence 30, Appl
5	436	96.5	398	4	US-09-291-417D-30	Sequence 30, Appl
6	436	96.5	591	3	US-09-082-737-2	Sequence 2, Appl
7	436	96.5	591	4	US-09-688-1888-103	Sequence 103, App
8	436	96.5	591	4	US-09-718-032-2	Sequence 2, Appl
9	436	96.5	591	4	US-09-291-417D-103	Sequence 103, App
10	436	96.5	591	4	US-09-949-016-6665	Sequence 6665, Ap
11	436	96.5	620	4	US-09-949-016-7206	Sequence 7206, Ap
12	379	83.8	681	4	US-09-688-1888-29	Sequence 29, Appl
13	379	83.8	681	4	US-09-291-417D-29	Sequence 29, Appl
14	379	83.8	694	4	US-09-949-016-10445	Sequence 10445, A
15	376	83.2	681	4	US-09-765-815-2	Sequence 2, Appl
16	277	61.3	244	3	US-09-163-507-2	Sequence 2, Appl
17	277	61.3	268	3	US-08-852-743-3	Sequence 3, Appl
18	277	61.3	268	3	US-09-185-370-3	Sequence 3, Appl
19	277	61.3	305	4	US-09-765-815-10	Sequence 10, Appl
20	277	61.3	465	2	US-08-114-555A-2	Sequence 2, Appl
21	277	61.3	465	3	US-08-559-397A-2	Sequence 2, Appl
22	277	61.3	545	4	US-09-538-092-1297	Sequence 1297, Ap
23	277	61.3	551	4	US-09-949-016-10951	Sequence 10951, A
24	276	61.1	245	3	US-09-163-507-3	Sequence 3, Appl
25	276	61.1	544	4	US-09-949-016-11562	Sequence 11562, A
26	276	61.1	545	2	US-08-935-760-4	Sequence 4, Appl
27	276	61.1	545	4	US-09-688-1888-93	Sequence 93, Appl

28	276	61.1	545	4	US-09-291-417D-93	Sequence 93, Appl
29	274	60.6	244	3	US-09-163-507-1	Sequence 1, Appl
30	274	60.6	524	2	US-08-615-942A-2	Sequence 2, Appl
31	274	60.6	524	4	US-09-237-325-2	Sequence 2, Appl
32	274	60.6	524	4	US-09-538-092-1301	Sequence 1301, Ap
33	274	60.6	544	2	US-08-935-760-2	Sequence 2, Appl
34	274	60.6	544	3	US-08-559-397A-19	Sequence 19, Appl
35	269	59.5	544	4	US-09-688-1888-95	Sequence 95, Appl
36	269	59.5	544	4	US-09-291-417D-95	Sequence 95, Appl
37	268	59.3	544	4	US-08-559-397A-30	Sequence 30, Appl
38	266	58.8	250	4	US-09-718-032-4	Sequence 4, Appl
39	266	58.8	506	1	US-08-369-780-2	Sequence 2, Appl
40	266	58.8	506	1	US-08-475-682-2	Sequence 2, Appl
41	266	58.8	506	1	US-08-780-833-2	Sequence 2, Appl
42	266	58.8	506	1	US-08-636-036-2	Sequence 2, Appl
43	266	58.8	506	3	US-08-918-509-2	Sequence 2, Appl
44	266	58.8	506	3	US-09-108-262-2	Sequence 2, Appl
45	266	58.8	506	4	US-09-688-1888-94	Sequence 94, Appl

ALIGNMENTS

```
RESULT 1
US-09-718-032-14
; Sequence 14, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/5311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718, 032
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082, 737
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 89
; TYPE: PRT
; ORGANISM: mouse
US-09-718-032-14

Query Match      100.0%; Score 452; DB 4; Length 89;
Best local Similarity 100.0%; Prod. No. 2,3e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQORRELFNEVIMRDYHENVNEMNSYLVGDELVMVMEFLGALTDIYTHTRMNEE 60
   |||||||
DB 1 KQORRELFNEVIMRDYHENVNEMNSYLVGDELVMVMEFLGALTDIYTHTRMNEE 60
   |||||||
QY 61 QIAAVCLAVLQALAVLHAQVTHSDIKTD 89
   |||||||
DB 61 QIAAVCLAVLQALAVLHAQVTHSDIKTD 89
   |||||||

RESULT 2
US-09-082-737-3
; Sequence 3, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NO. 6013500e1 Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
```

```
COUNTRY: U.S.A.
ZIP: 11230
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,737
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-082-737-3
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```
Query Match          96.5%; Score 436; DB 3; Length 250;
Best Local Similarity 95.5%; Pred. No. 1e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 60
DB 33 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 92
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 93 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 121
```

```
RESULT 3
US-09-718-032-3
Sequence 3, Application US/09718032
Patent No. 6667168
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: Minden, Audrey
TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
FILE REFERENCE: 575/55311-A-PCT-US
CURRENT FILING DATE: 2000-11-21
CURRENT APPLICATION NUMBER: US/09/718,032
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 09/082,737
PRIOR FILING DATE: 1998-05-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 250
TYPE: PRT
ORGANISM: human
US-09-718-032-3
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```
Query Match          96.5%; Score 436; DB 4; Length 250;
Best Local Similarity 95.5%; Pred. No. 1e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 60
DB 33 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 92
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 93 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 121
```

```
DB 93 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 121
RESULT 4
US-09-688-188B-30
Sequence 30, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT FILING DATE: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR FILING DATE: 09/291,417
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-688-188B-30
```

```
Query Match          96.5%; Score 436; DB 4; Length 398;
Best Local Similarity 95.5%; Pred. No. 2e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 60
DB 163 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 222
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 223 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 251
```

```
RESULT 5
US-09-291-417D-30
Sequence 30, Application US/09291417D
Patent No. 6680170
GENERAL INFORMATION:
APPLICANT: PLOMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT FILING DATE: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
PRIOR FILING DATE: 09/081,784
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-291-417D-30
```

```
Query Match          96.5%; Score 436; DB 4; Length 398;
Best Local Similarity 95.5%; Pred. No. 2e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 60
DB 163 KOORRELFNEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVTTRNNEE 222
QY 61 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 89
DB 223 QIAAVCLAVLQALAVLHAQGVHSIDIKTD 251
```


RESULT 6
US-09-082-737-2
; Sequence 2, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4; A NO. 6013500el Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-082-737-2

Query Match 96.5%; Score 436; DB 3; Length 591;
Best Local Similarity 95.5%; Pred. No. 3.4e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVYHTRMEE 60
|||
DB 356 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVYHTRMEE 415
|||

QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
|||
DB 416 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 444
|||

RESULT 7
US-09-688-188B-103
; Sequence 103, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-103

Query Match 96.5%; Score 436; DB 4; Length 591;
Best Local Similarity 95.5%; Pred. No. 3.4e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVYHTRMEE 60
|||
DB 356 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVYHTRMEE 415
|||

QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
|||
DB 416 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 444
|||

RESULT 8
US-09-718-032-2
; Sequence 2, Application US/09718032
; Patent No. 6667168
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
; FILE REFERENCE: 575/55311-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/718,032
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: PCT/US99/11341
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/082,737
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 591
; TYPE: PRT
; ORGANISM: human
US-09-718-032-2

Query Match 96.5%; Score 436; DB 4; Length 591;
Best Local Similarity 95.5%; Pred. No. 3.4e-47;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVYHTRMEE 60
|||
DB 356 KOORRELFENEVIMRDYHENVEMNSYLVGDELMVMEFLGGALTDIVYHTRMEE 415
|||

QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
|||
DB 416 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 444
|||

RESULT 9
US-09-291-417D-103
; Sequence 103, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591

TYPE: PRT
ORGANISM: Homo sapiens
US-09-291-417D-103

Query Match
Best Local Similarity 96.5%; Score 436; DB 4; Length 591;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
DB 356 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 415
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 416 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 444

RESULT 10
US-09-949-016-6665

Sequence 6665, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6665
LENGTH: 591
TYPE: PRT
ORGANISM: Human
US-09-949-016-6665

Query Match
Best Local Similarity 96.5%; Score 436; DB 4; Length 591;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
DB 356 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 415
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 416 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 444

RESULT 11
US-09-949-016-7206

Sequence 7206, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7206
LENGTH: 620
TYPE: PRT
ORGANISM: Human
US-09-949-016-7206

Query Match
Best Local Similarity 96.5%; Score 436; DB 4; Length 620;
Matches 85; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
DB 385 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 444
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 445 QIAAVCLAVLQALAVLHAQGVTHSDIKSD 473

RESULT 12

US-09-688-188B-29
Sequence 29, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICHARD
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 681
TYPE: PRT
ORGANISM: Homo sapiens
US-09-688-188B-29

Query Match
Best Local Similarity 83.8%; Score 379; DB 4; Length 681;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 60
DB 442 KQRRLLFNEVIMRDYRHHENVEMVNSYLVGDELMVMEFLGGALTDIVTHTRMNEE 501
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 502 QIAVCEAVLQALAVLHAQGVTHSDIKSD 530

RESULT 13

US-09-291-417D-29
Sequence 29, Application US/09291417D
Patent No. 6680170
GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICHARD
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 29
LENGTH: 681
TYPE: PRT
ORGANISM: Homo sapiens
US-09-291-417D-29

Query Match 83.8%; Score 379; DB 4; Length 681;
Best Local Similarity 83.1%; Pred. No. 8, 2e-40;
Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVVIKRDYRHEVNVEMVNSYLVGDELAVVMEFLGGALTDIVYTHRRMEE 60
DB 442 KOORRELLFNEVVIKRDYRHEVNVEMVNSYLVGDELAVVMEFLGGALTDIVSQRVLRNEE 501
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 502 QIATVCEAVLQALAVLHAQGVTHSDIKSD 530

RESULT 14
US-09-949-016-10445

Sequence 10445, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10445

LENGTH: 694

TYPE: PRT

ORGANISM: Human

US-09-949-016-10445

Query Match 83.8%; Score 379; DB 4; Length 694;
Best Local Similarity 83.1%; Pred. No. 8, 4e-40;

Matches 74; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVVIKRDYRHEVNVEMVNSYLVGDELAVVMEFLGGALTDIVYTHRRMEE 60
DB 455 KOORRELLFNEVVIKRDYRHEVNVEMVNSYLVGDELAVVMEFLGGALTDIVSQRVLRNEE 514
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 515 QIATVCEAVLQALAVLHAQGVTHSDIKSD 543

RESULT 15

US-09-765-815-2

Sequence 2, Application US/09765815

Patent No. 6673586

GENERAL INFORMATION:

APPLICANT: Baik, Steven

TITLE OF INVENTION: No. 6673586e1 Steroid Hormone Receptor

FILE REFERENCE: 01948/068002

CURRENT APPLICATION NUMBER: US/09/765,815

PRIOR FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: US 60/176,859

PRIOR FILING DATE: 2000-01-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 681
TYPE: PRT
ORGANISM: Homo sapiens
US-09-765-815-2

Query Match 83.2%; Score 376; DB 4; Length 681;
Best Local Similarity 82.0%; Pred. No. 2e-39;
Matches 73; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KOORRELLFNEVVIKRDYRHEVNVEMVNSYLVGDELAVVMEFLGGALTDIVYTHRRMEE 60
DB 442 KOORRELLFNEVVIKRDYRHEVNVEMVNSYLVGDELAVVMEFLGGALTDIVSQRVLRNEE 501
QY 61 QIAAVCLAVLQALAVLHAQGVTHSDIKTD 89
DB 502 QIATVCEAVLQALAVLHAQGVTHSDIKSD 530

Search completed: March 15, 2005, 11:32:29
Job time : 7.85294 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 11:16:56 ; Search time 44.325 Seconds

(Without alignments)
1282.890 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090
Sequence: 1 MGCKKKRVEISAPSNFEHR.....LAKAGPPASIVPLMRQNR 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1096.5	35.5	540	2	TI9956 hypothetical prote
2	1090.5	35.3	542	2	TI9952 hypothetical prote
3	917	29.7	544	2	A57597 beta-p21-activated
4	907	29.4	544	2	I49376 p21 activated kina
5	895.5	29.0	525	2	S58682 protein kinase, p2
6	892.5	28.9	545	2	G01773 p21-activated prot
7	892	28.9	544	2	S40482 serine/threonine-s
8	846.5	27.4	1230	2	T18256 probable serine/th
9	846.5	27.4	1230	2	T18259 serine/threonine p
10	837	27.1	939	2	S28394 probable serine/th
11	823.5	26.7	658	2	T39500 serine/threonine-s
12	814.5	26.4	658	2	S60170 protein kinase Pak
13	811.5	26.3	622	2	T15467 hypothetical prote
14	760	24.6	842	2	S60402 protein kinase CLA
15	722	23.4	378	2	T26684 hypothetical prote
16	697	22.6	589	2	T38086 serine/threonine-p
17	651.5	21.1	655	2	S51884 probable protein k
18	505	16.3	836	2	B96716 probable serine/th
19	498	16.1	471	2	T39322 probable serine th
20	494	16.0	1102	2	JC6316 hypothetical prote
21	478	15.5	653	2	T34356 hypothetical prote
22	476	15.4	819	2	A53714 protein kinase (EC
23	470.5	15.2	829	2	T29372 hypothetical prote
24	464	15.0	426	2	S71886 Ste20-like protein
25	463	15.0	1231	2	T18532 serine/threonine pr
26	462	15.0	1233	2	T14157 serine/threonine p
27	460	14.9	1206	2	T34021 protein kinase SK2
28	458.5	14.8	690	2	C96572 protein F12M16.4 l
29	455.5	14.7	1080	2	S48944 hypothetical prote

30	455	14.7	1233	2	T30989 serine/threonine p
31	450.5	14.6	312	2	T38525 serine/threonine p
32	444.5	14.4	1001	2	T17365 serine/threonine p
33	440.5	14.3	1075	2	T27623 hypothetical prote
34	440.5	14.3	1080	2	T27622 hypothetical prote
35	437.5	14.2	1062	2	S46367 protein kinase CDC
36	428	13.9	1228	2	T18897 hypothetical prote
37	424.5	13.7	659	1	A39723 protein kinase bcr
38	421	13.6	553	2	T01479 hypothetical prote
39	419	13.6	883	2	A96662 hypothetical prote
40	417.5	13.5	1174	2	T43051 protein kinase C (
41	413	13.4	561	2	T51417 protein kinase-1lk
42	409.5	13.3	652	2	T39722 serine/threonine p
43	409	13.2	891	2	T40503 protein kinase kin
44	405.5	13.1	1139	1	S61918 protein kinase C (
45	404.5	13.1	1135	1	A29813 132k nlmac protein

ALIGNMENTS

RESULT 1

TI9956 hypothetical protein C45B11.1b - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 16-Aug-2004

C/Accession: TI9956

R/McMurray, A.

A/Reference number: Z19202

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-540 <MIL>

A/Cross-references: UNIPROT:Q9U3M1; EMBL:Z74029; PIDN:CAA98433.1; GSPDB:GN00023; CESP:C

A/Experimental source: clone C45B11

C/Genetics:

A/Map position: 5

A/Intons: 13/2; 62/3; 104/2; 231/3; 367/2; 468/3

C/Superfamily: protein kinase homology

Query Match	Score	Length	DB 2	Length	DB 1
Best Local Similarity	41.7%	Pred. No. 4.1e-31;			
Matches 251; Conservative 67; Mismatches 151; Indels 133; Gaps 9;					
QY	4	KKKRVEISAPSNFEHRVHTGFDHOKFTGHPQWQSLI--EESARRKPLVDPACITS	61		
DB	29	KVKKSEISTPNSFEHRIHAGFDARSGTYTGLPKQWQALLGPPRSISRKPMVDPSCTIP	88		
QY	62	IQGADKTVKSGKAGDGLTLLDEFENMSVTRNSLRDSPPPPARARQENGMPEEP	121		
DB	89	VVAELKTVIRGSSRYNSPLPFGMTNSPMPVSARSNSIRISKTASP-----	135		
QY	122	ATTARCGPKAGSRGFFAHSEACGGSGRRRAAGPRKRSSESGCGQESGRDRPLPS	181		
DB	136	-----VVNVSAHSPFPLPVSPQ-----	156		
QY	182	GPVDVTPDAGLASGAKLAGRPFTYPRADTDHPSRGAQGBHDVAPNPSAGLAIHQ	241		
DB	157	-----GYPF-----NDPVAFLPL--	170		
QY	242	SSSSSRPPTRRAGAPSGVLAGPH-----ASEPOLAPACTPAAPAVGPPG	288		
DB	171	---RNQKPPM---STTFGEVKEPHOYQIITIVASRTTTPOLQPKS-----PST	213		
QY	289	PSAPQREP---QVSHSEGFRAQLQVVDGDSRYLDNFKIGESGTGIVCIATVRSQK	345		
DB	214	PQMRQQPKCTGSGVSDSEFRNALKFPVDSGTDSDTLTKQIGEGSGVGAAYKISTNQ	273		
QY	346	LVAVKMDLRKQORRELLFNEVYIMBDYOHENNVEMVYNSLVGDELVMVMEFLGGALTD	405		
DB	274	IYAVVRMNLKQQRRLLEFNEVSIIRQYOHPIVIRFFSHLVLDDELVMVMEFEGSLTD	333		

QY 406 IYTHIRMEBOIAVCLATLQALSVLHAQGVTHRDIKSDSILLTHDGRVYKLSDFGFCQAY 465
Db 334 IYATATRMTEPQIATISRQVLGALDFLHARKVTHRDIKSDSILLKRDGVTKLDFGFCQGL 393
QY 466 SKEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSIGIWIEMVDEGPEPFYNEPPLKAMK 525
Db 394 SEEVPRRRSLVGTPTWTAELVAREPYDTRADISFGMLIEMVGEDEPFNDQFQAMK 453
QY 526 MIRDLNLPRLKNLHKVSPSLKGFDLRLVDRPAQATAAELIKHPFLAKAGPPASIVPLM 585
Db 454 RIRDEHEARFBRHAKVSELSSELISHCIYDVNKRWPADLRLRHPFAKQHSSTIAPLL 513
QY 586 RQ 587
Db 514 LQ 515

RESULT 2
T19952
hypothetical protein C45B11.1a - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C/Accession: T19952
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z19202
A/Accession: T19952
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-542 <M1>
A/Cross-references: UNIPROT:Q18637; EMBL:Z74029; PIDN:CAA98429.1; GSPDB:GN00023; CESP:C4
A/Experimental source: clone C45B11
C/Genetics:
A/Gene: CESP:C45B11.1a
A/Map position: 5
A/Intons: 13/2; 62/3; 104/2; 233/3; 369/2; 470/3
C/Superfamily: protein kinase homology

Query Match 35.3%; Score 1090.5; DB 2; Length 542;
Best Local Similarity 42.0%; Pred. No. 6, 6e-31;
Matches 253; Conservative 69; Mismatches 149; Indels 131; Gaps 11;

QY 4 KKKRVEISAPSNFEHNVHGFDPQHEQKFTGLPRMOSLI--ESARRPKPLVDPACTIS 61
Db 29 RKVKSEISLSPSEFHHIAGFDARSCTYGLPKQMLGPPRSISRKEMWDSCTTP 88
QY 62 IOPGAKTIVRSGKAGDGLTLTLDDEFENSVTRNSLRRDSPPPAPARQENGPEEP 121
Db 89 VDVAEKTYLRGP-----SSFRVNSPLP-----FGMTNSP 119
QY 122 ATTARGGPGKAGRGPFAGHSEAGSGGDRRRRAGPEKRPKSSRSGSGFQESSRDRKPLS 181
Db 120 MPEV---ARSNLSIRSATASPVNVNVSARHSFRPLPVSQR----- 158
QY 182 GPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVAAPNGPSAGLAIQ 241
Db 159 -----GYPF-----NDPSIAPLPL-- 172
QY 242 SSSSSSRPPTRAGAPSPVLAGPH-----ASBPOLAPACTPAAAPVAGPBG 288
Db 173 ---RNQKPRM---STTFGEKPHQYQOITITVAERSTTPQIQPKS-----PST 215
QY 289 PRSPQREP---QVSHQEPFAALQLVVDPEDPSTYDNFKIGSGTGIVCIATVRSQK 345
Db 216 PQAMROQPKCTEGVSEEFNALKFVVDGTDPRSDDLTYKQIGEGSTGVVEAAYKISTQ 275
QY 346 IYAVKQMDLRKQORRELFNEVYIMRDYOHENNVEMVNSYLVGDELAVVMEFLGEGALND 405
Db 276 IYAVKQMDLRKQORRELFNEVYIMRDYOHENNVEMVNSYLVGDELAVVMEFLGEGALND 335
QY 406 IYVHTMNEBOIAVCLATLQALSVLHAQGVTHRDIKSDSILLTHDGRVYKLSDFGFCQAY 465

Db 336 IYATATRMTEPQIATISRQVLGALDFLHARKVTHRDIKSDSILLKRDGVTKLDFGFCQGL 395
QY 466 SKEVPRKSLVGTPTWMAPELISRLPYGPEVDIWSIGIWIEMVDEGPEPFYNEPPLKAMK 525
Db 396 SEEVPRRRSLVGTPTWTAELVAREPYDTRADISFGMLIEMVGEDEPFNDQFQAMK 455
QY 526 MIRDLNLPRLKNLHKVSPSLKGFDLRLVDRPAQATAAELIKHPFLAKAGPPASIVPLM 585
Db 456 RIRDEHEARFBRHAKVSELSSELISHCIYDVNKRWPADLRLRHPFAKQHSSTIAPLL 513
QY 586 RQ 587
Db 516 LQ 517

RESULT 3
A57597
beta-p21-activated protein kinase - rat
N/Alternate names: beta-PAK
C/Species: Rattus norvegicus (Norway rat)
C/Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C/Accession: A57597
R:Maner, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L.
J. Biol. Chem. 270, 25070-25078, 1995
A/Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) f
A/Reference number: A57597; MUID:96027610; PMID:7559638
A/Accession: A57597
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-544 <MAN>
A/Cross-references: UNIPROT:Q62829; GB:U33314; NID:91039424; PIDN:AAC52268.1; PID:910394
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C/Keywds: ATP
F/266-518/Domain: protein kinase homology <KIN>
F/274-282/Region: protein kinase ATP-binding motif

Query Match 29.7%; Score 917; DB 2; Length 544;
Best Local Similarity 35.8%; Pred. No. 5, 2e-25;
Matches 211; Conservative 87; Mismatches 165; Indels 126; Gaps 8;

QY 4 KKKRVEISAPSNFEHNVHGFDPQHEQKFTGLPRMOSLI-----ESARRPKPLVDP 56
Db 63 KEKERPEISLSPDEPHITVGFDAVTEFTGIPQWMLTQTSNITKLEQKKNQAVLD- 121
QY 57 ACTISIGGAKTIVRSGKAGDGLTLTLDDEFENSVTRNSLRRDSPPPAPARQENG 116
Db 122 -----VLKPYSKETVNNQKMSFT----- 141
QY 117 MPEEPATTARAGPGKAGRGPFAGHSEAGSGGDRRRRAGPEKRPKSSRSGSGFQESSRD 176
Db 142 -----SGDKSAHGYIAAHQ-----SNKTKASERPLAPVSEDEDEEEDD 184
QY 177 KRPISGPDVGTTPQAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPHDVAAPNGPSAG 236
Db 185 NEP---PVIAPRPETHS-----IYTSVVSISAP-----APNKEATRP 223
QY 227 LAIPQSSSSSRPPTRAGAPSPVLAGPHASEPQALAPACTPAAAPVAGPBGSPQREP 296
Db 224 SAENANSSSTLYRNDK-----QKK 243
QY 297 QVSHQEPFAALQLVVDPEDPSTYDNFKIGSGTGIVCIATVRSQKLAIVKQMDLRK 356
Db 244 SKMTDEBELLEKRSIVSGDPKKYTRREKIKGGASGVYVYALDIATQGEVAILQMDLQ 303
QY 357 QQRRELFNEVYIMRDYOHENNVEMVNSYLVGDELAVVMEFLGEGALNDIYTHIRMEBO 416
Db 304 QPKKELIINEIIVMENKQNPINIVNLDISYLVGDELAVVMEFLGEGALNDIYTHIRMEBO 363
QY 417 IYAVCLATLQALSVLHAQGVTHRDIKSDSILLTHDGRVYKLSDFGFCQAYVSKVPRKSLV 476
Db 364 IYAVCECQALDFHSHQVTHRDIKSDSILLGMDSGYKLDYFGCAQITTEBQSGKSTNV 423
QY 477 GTPYMAPELISRLPYGPEVDIWSIGIWIEMVDEGPEPFYNEPPLKAMKMIKMDLNPRLK 536

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Db      424 GPTVMAPEVVTIKKAGPKVDIWSLGIWAIEMWBEPYLAENPRALYLITNGTPELQ 483
Oy      537 NLHKVSPSLKGFLDRLIVRDPACRATAAELLKHPLAKGAPPAIVPLM 585
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      484 NPERLSAVFPDFLNRCLEMDVDRSGAKELLQHPLKLAKPLSSLTPLI 532

RESULT 4
149376
P21 activated kinase-3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C:Accession: I49376
R:BAGRODIA, S.; TAYLOR, S.J.; CREASY, C.B.; CHERNOFF, J.; CERTONE, R.A.
J: Biol. Chem. 270, 22731-22737, 1995
J>Title: Identification of a mouse p21cdc42/Rac activated kinase.
A:Reference number: I49376; MUID:96032693; PMID:7555398
A:Accession: I49376
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-544 <RES>
A:Cross-references: UNIPROT:Q6I036; EMBL:U39738; NID:g1079713; PION:AAC52354.1; PID:g107
A:Gene: mpk-3
C:Superfamily: protein kinase homology
C:Keywords: ATP
F:266-519/Domain: protein kinase ATP-binding motif
F:274-282/Region: protein kinase ATP-binding motif

Query Match          29.4%; Score 907; DB 2; Length 544;
Beat Local Similarity 34.6%; Pred. No. 1.1e-24;
Matches 204; Conservative 90; Mismatches 169; Indels 126; Gaps 7;

Oy      4 KKKRRVEISASPMFEHRVHTGFQDEQKFTGLPPROMOSLIE-----ESARRPKRVLP 56
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      63 KEKEREELSPDSPEHITHVGFDVATGBETGTIGEWARLLQTSNITKLGKQNPOAVLD- 121
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      57 ACITSIQPGAKPIVRGSKAKODALTLLDEFENSTYRSNSLRDSPPPARAQENG 116
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      122 -----VLKFYSKEVNNQKMSFT----- 141
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      117 MEPEPYTTARGFGKAGSRGRFAGHSEAGGGSGDRRRAPGEKRPKYSRGSGGPQESSND 176
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      142 -----SGDKSAHGVIYAHQ-----SNTKTGSEPLAPVSEDEDEEEEDDD 184
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      177 KKPPLSPDVGTPOPAGLASGAKLAGRPENTYPRAADTHPSRGAQGEBPDVAVPNGSSAG 236
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      185 NEP---PPVIAAPREPHTKS-----LYTRSVSESIASPAANKKDIPPSSANENS 230
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      237 LAIPOSSSSSSRPPTRARGAPSPGVLPGRHASEPOLAPACTPAAPAVPQPGRSPQREP 296
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      231 TTLRYNRTR-----QRKK 243
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      297 QRVSHQFOFRALQLVNDPCGPSYLDNFIRKIGEGSTGIVCIATVRSQGLVAVKQNDLK 356
|       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      244 SKMTDEILIEKMSIVSGDPKKYTRLEKIQQGASGVYYRALDIATGTEVALIKQNNLQ 303
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      357 QQRRELLFNEVIMRDYQHEHVEMTNSYLVGDELVMMEFLGEGALLTDIVYHTRMNEQ 416
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      304 QPKKELLINELVMRENKNPRIIVYLLSYLVGDELMVMMEYLAGSLLTDVVVETCTCDVQ 363
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      417 IAAVCLAVIALSVLHAQGYIHRDIKSDSILLTHDGRVYLSDFGCAGVSKVPRKSLV 476
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      364 IAAVCEBCIALDLFHSNOVIHRDIKSDNILMGDGSVKLTDIFGCCAQITTPSQSKSTNV 423
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      477 GTPYMAAPELISRLPVGEVDIWSLGINVIEWDGEPFYFNPPKAMKMRINDLPPRLK 536
|       |||||:::||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      424 GTPYMAAPEVVTIKKAGPKVDIWSLGIWAIEMWBEPYLAENPRALYLITNGTPELQ 483
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      537 NLHKVSPSLKGFLDRLIVRDPACRATAAELLKHPLAKGAPPAIVPLM 585
|       |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      484 NPERLSAVFPDFLNRCLEMDVDRSGAKELLQHPLKLAKPLSSLTPLI 532

```

RESULT 5

558682

protein kinase, p21-activated (EC 2.7.1.-) - human

N:Alternate names: protein kinase PAK65; S6/H4 kinase

C:Species: Homo sapiens (man)

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004

C:Accession: S58682; S55258; S55304; S58690; A57441

C:Submitted to the EMBL Data Library, April 1995

A:Description: Human p21-activated protein kinases regulate actin organization in mammal

A:Reference number: S58682

A:Accession: S58682

A:Molecule type: DNA

A:Residues: 1-525 <SEL>

A:Cross-references: UNIPROT:O13177; EMBL:U24153; NID:G780807; PIDN:AAA65442.1; PID:G7808

R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 1970-1978, 1995

A:Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation 1

A:Reference number: S55258; MUID:95262637; PMID:7744004

A:Accession: S55258

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 'MERTQKSNLEL', 31-89, 'T', 91-149, 'F', 151-224, 'T', 226-328, 'R', 330-338, 340-525

A:Accession: S55304

A:Molecule type: protein

A:Residues: 402-418 <MAM>

R:Martin, G.A.; Bollag, G.; McCormick, F.; Abo, A.

EMBO J. 14, 4385, 1995

A:Reference number: S58690; MUID:96016211; PMID:7556080

A:Contents: erratum

A:Accession: S58690

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

R:Benner, G.E.; Dennis, P.B.; Mataracchia, R.A.

J. Biol. Chem. 270, 21121-21128, 1995

A:Title: Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular an

A:Reference number: A57441; MUID:95403344; PMID:7673144

A:Accession: A57441

A:Molecule type: protein

A:Residues: 197-216; 402, 'S', 404-409 <BEN>

A:Experimental source: placenta

C:Superfamily: protein kinase homology

C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonin

F:247-501/Domain: protein kinase homology <KIN>

F:255-263/Region: protein kinase ATP-binding motif

F:197,402/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 29.0%; Score 895.5; DB 2; Length 523;

Best Local Similarity 34.9%; Pred. No. 2,7e-24;

Matches 211; Conservative 94; Mismatches 136; Indels 163; Gaps 14;

4 KRKKVETASAPENFEHRYVTGPDHOKFTGTLPROMOSLIE-----ESARRPKPLVDP 56

67 KEKERPEISPPEDFEHTIHVGFDAVTEGTFMGPEQMARLLQTSYITLLEQKQKQPAVD 125

57 ACTISIQPAPXTIVRGSKAGDALLTLIDFEENNSVTRSNLSLRD--SPPPARAROE 114

126 -----VLKPYD-----SNTVKKQYLSFTPP---EK 147

115 NGMPR-EPATTARGGPGKAGRGFRFAGHSAGGSGDRRARAPRKPKRSSESGGSGPOES 173

148 DGLPSTPLANKG-----TEA-----DAVTEEDDDDET 178

174 SRDKRPLSGPDVGTGPAGIAGAKLAAGRPFTYPRADTDHPSGAQGEHDAVPNGPS 233

179 A-----PPIYADRPDHTKS-----IYRSVID-PVPAPVGDH----- 210

234 AGGLAIPOSSSSSSRRPTTARAGAPSGVGLGPHASPEQLAPRACTPAARPAVPGPGRSPQ 293

211 -----VDGAAKSLDKQ 221

[illegible]

RESULT 6

P21-activated protein kinase - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
 C:Accession: G01773
 R:Chernoff, J.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: G08374
 A:Accession: G01773
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-545 <CHE>
 A:Cross-references: UNIPROT:Q13153; EMBL:U024152; NID:g780805; PIDN:AA65441.1; PID:g780805
 C:Genetics:
 A:Gene: Pak1
 C:Superfamily: protein kinase homology
 ;268-521/Domain: protein kinase homology <KIN>

	Query Match	28.9%	Score 892.5	DB 2	Length 545,
	Betw Local Similarity	36.9%	Pred. No. 3.5e-24,		
	Match 216; Conservative	82;	Mismatches 166;	Indels 121;	Gaps 11;
Qy	4 KRRKRVEISAPSNPEHRVHTGPDHQEQQFTGLPROMOSLIBESARPKPLVDPACTSIQ	63			
Db	68 KEKERPEI SLSDPFHITLHVGFDAVTGEFTGNPEGMARLLQTSN-----	111			
Qy	64 PGAPKTYRGSKGADGALLTLIDFEFENMSTRNSLRDSEPPPARAKENGMPPEPAT	123			
Db	112 -----ITYSEOKKNPOAVLDIVLEFYNSKYT-SNSQCKMS-----	144			
Qy	124 TARGGPGAGAGRPRAGHSBAGCGSGDRRRAPGERPRKSREGSGCPQESSRDKRPLSGP	183			
Db	145 -----FTDKSAEDYNSNLANLV-----RAVSETPAVPVSDEED-DDD	181			
Qy	184 DVGTPEOPAGLASGAKLAGRPENT--XPRADTDHPSRGAGEPHDVAPNGBSAGLAIP	240			
Db	182 DDATPPP-----VIAPREHNTSVSTRSL-----ELPLPVPT-----	214			
Qy	241 QSSSSSRPPTRFARGCAPSPGVLGPHASEQLAPPACTPAAPVAGPGRSPQOREPQVS	300			
Db	215 RDVATSPISEPINTTP-----PDALTINT-----EKOKKKPKMS	249			
Qy	301 HEQFPAAALQWDPEDPRSLYDNFKIKIGBSTGYCIATVSSGGVLVAVKMKDLRKQQR	360			
Db	250 DEILETEKRSIVSDDPKKRYTRFERKIQQGASGYTTAMDVADEVAIKOMNLDOOEPK	309			

Oy		36	ELLFNEVIMRBYOHENHVEKMSNLSVLDEDELAVMEFELEGGLADITHIRNMIEBOIAAY	420
Db		310	ELIINELWREKKKNPNIYNITDLSLVEDELAVMEYIAGSLDVDTEICMBEGOIAAV	369
Oy		421	CLAVLOALSVLAHOQVIHRDIKSDSILLTHDRGKYSDFGCACVSKEVRPKSLVGTPY	480
Db		370	CRCLOALEFLHSNQIVIHHDIKSDNITLLGMDSVKYLDNFGCAITPEGRKSTWGTGY	429
Oy		481	WMAPELISRLPYGPFEVDIWSLGIMVILEVNDGEPPRYNBPPLKANKMTKDMLPRILKYLK	540
Db		430	WMAPEVVTERRAKGPKVIDMISLGIMAIEMIBESPPILENPPLRALYLLATNGTPELOAPEK	489
Oy		541	VBSLSLKGFLDLLVMDPQRATPAEALLGHPRFLAAGPASPASIVPM	585
Db		490	LSAIFPDPLNRCLMDIVEGRSGASELLOHQPLKTAKPUSSTLTPII	534

RESULT 7

C:serine/threonine-specific protein kinase (EC 2.7.1.1) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #tex_change 16-Aug-2004
C:Accession: S40482
R:Manseer, B.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.
Nature 367, 40-46, 1994
A:Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.
A:Reference number: S40482; MUID:94150588; PMID:8107774
A:Accession: S40482
A:Molecule type: mRNA
A:Residues: 1-544 <MAN>
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:267-520/Domains: protein kinase homology <KIN>
F:275-283/Region: protein kinase ATP-binding motif

Query Match	28.9%;	Score 892;	DB 2;	Length 544;
Best Local Similarity	36.9%;	Pred. No. 3.6e-24;		
Matches 216;	Conservative 82;	Mismatches 165;	Indels 122;	Gaps 11;

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OY KRKRVEIASPNFHRVYTGDDHEOEKOTLPRWOMOLIEESARRKPLVDPACITSIQ 63
Db KEKERHEISPSDFEHTTHVGFDPACTGEFTGMPEOMARLIOTSU----- 111
OY 64 PGAPKTYVGSXKAGKALTLLDDEFEMSWYTRSNSLRDSPPPPARAOENGMPPEPAT 123
Db 112 -----IKTSQGNKPQAVLDVLEFYNSKCT-SNSQKXMS----- 144
OY 124 YARGPGKAGSKRGPRFAGHSAGSGSGDRRRAGPEKRPKSSREGSGGQESSRKRPLSGP 183
Db 145 -----FDDKSAEDYNSNTLANY-----KTVSETPAVPVSEDE-----DD 180
OY 184 DVGTPOGAGLASGAKLAAGRPENT---YPRADTDHPKSGAQGEPHDVAHPGSPAGGLAIP 240
Db 181 DDATPPP-----VIAPREHTKSVYTRSVI-----ELPLPTPT----- 213
OY 241 QSSSSSRPPTARGAPSEFVLGPHASEPOLAPACTPAAVAPGPPGPPSPQREPORVS 300
Db 214 RDVATEPISPTENTTP-----PDALTFRNT-----EKQKKXPXMS 248
OY 301 HEOFRALQULVDPGDPRSVDLNFITKIGBSGTGYCIATYRBSGKLYAVYKMDLRKQOR 360
Db 249 DEELTEKLRNIVSVDGPKKRYTRFEFKIQGASGVLYTAMDVATQGEVAIKOMLQOQPKK 308
OY 361 ELLFNEVYIMRDVOGHENNVEMNSYLVGDELMVYMEFLFEGALTDIYTHRRNBEOLAAV 420
Db 309 ELLINELIYVRKEKNKNVINYLDSTLVGBZELVVMVEYIAGASGLTDVITFCMBEGQIAAV 368
OY 421 CLAVLOALSTVHAQGYIHRDIKSDSYILLTHDGRVYLSDFGCACAVSKVEPRKSLVGPY 480
Db 369 CRECLQALERTHSNQYIHRDIKSDYILLGMSGSVYLTDFGCAQITDFQGRBSRSMVGPY 428
OY 481 WMAPELISRLPYGPEVDWISGIMVYIEWVDGEPYFNEPPLKAMKMTIDNLPPRLKYLHK 540

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Db 429 WMAPEVTRKAYGPKVDIWSLIGIMALEMIGEPPEYLINENLRALYLATNGTELOQPEK 488
QY 541 VSPSLGFLDRLLVRDPAQATAAEILKHPFLAKAGPASIPLM 585
Db 489 LSAIFRDFLNRCLMEVDKRSKAKELLQHFLLKIAFLSLTPLI 533

RESULT 8

T18256
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - yeast (Candida albicans)
C/Specter: Candida albicans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18256
R/Leberer, E.; Harcus, D.; Broadbent, I. D.; Clark, K. L.; Dignard, D.; Ziegelbauer, K.; S
Proc. Natl. Acad. Sci. U.S.A. 93, 13217-13222, 1996
A/Title: Signal transduction through homologs of the Ste20p and Ste7p protein kinases ca
A/Reference number: Z18843; PMID:97075145; PMID:8917571
A/Accession: T18256
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1230 <LEB>
A/References: UNIPROT:O13431; EMBL:L47210; NID:g2276410; PID:g2286042; PIDN:AA8654
C/Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 27.4%; Score 846.5; DB 2; Length 1230;
Best Local Similarity 27.1%; Pred. No. 2.4e-22;
Matches 221; Conservative 114; Mismatches 220; Indels 259; Gaps 17;

QY 1 MFGKRRK-----RVEISAPSNFEHRVATGFDHOKFTGLPRQWGL 42
Db 447 MFGKNTSTSSSSSGNSHSGQEVNIKISTFNAKHLAVGIDN-GSYTGLPIEMERL 505
QY 43 I-----ESARRPPVLDPACT--TSIQCAPRTIYVSGKAGDGLTLLDPEFM 92
Db 506 LSAIGITKKEQOHPQAVMDIVAFOYDTSEN-----DDAFAKFE--HFDNN 550
QY 93 SVTRSNLSLRDSP-----PPARAENGMEEPATYARG 128
Db 551 KSSSSGMSMENTPPATPPGSSNGSGSGGAGAPSSPHRTPPSIIENKNVEQKYYTSSQM 610
QY 129 PGKAGRGPRAGHSEAGGSGDRRRAGPEKRPKS--REGSGGPOESS--RDKRPLSGPDV 185
Db 611 PRTTESK-----QSENHQPHEDNATQYTRPTFSHVQEGQFIPSRAPKRPSTPLSSMSV 665
QY 186 GTPQAPGLASGAKLAAGRPNTYPPRADTDPHSGAGCEPHD----- 226
Db 666 SHKTPSS-----QSLPRSDSQSDIRSTRPKSHQDVSPSKIKIRISISKSLKS 712
QY 227 -----VAPNGPSAGLAIPQSSSSSRPTPRAGAPSPVLAGP----- 264
Db 713 MRSKSGDKFTTHIAPRPPPSLPSIPKSKSHSASLSQLRPATNGSTTAPIPASAAFGGE 772
QY 265 -----HASEPQLAPACTPAAPAVPGPP----- 287
Db 773 NNALPKQRIINEFKAHAPR--PPPSAPRPPRPPRANULSQTSEIPQORTAPSGALA 830
QY 288 ----- 287
Db 831 DVTAPNTIYEIOQTKYQEAQOKLREKKALEBEIOLREKNERONROQETGQNNADTAG 890
QY 288 -----GPRSP-----OREPQVSHQEPRAALQOLVDDGDP 318
Db 891 GSNIAFPVPPVPPKPPSGSGGGRDAKOALLIAQKKEBKRRKQLQIIAKLKTICNRPDP 950
QY 319 SYLDNFIKIGEGSTGIVCIA-TVRSAGKLVAVKMDLRKQORRELLFNEVIMRDYOHEN 377
Db 951 ELYVDLVKIGQAGSGGVFLAHVDVRDKNIVAIKQNMLEQPKKELLINELIVKSGSSHN 1010
QY 378 VEMNYSYLVGDLVAVMEFLBEGALTDIYTRANBEQIAVAVCLAVLQALSTLHAGCY 437
Db 1011 IYVFIISYLLKGLLWIMETMEYBEGSLDIYTHGVMTEGOIGVVCREFLKLKFLHSGVY 1070
QY 438 HRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTWMAPELISRLPYGPEVD 497

Db 1071 HRDIKSDNILLNMDGNIKITDFGCAQINEINSKRITTMGTPTWMAPEIYSRKEGPKVD 1130
QY 498 INSIGIMVEMDGEPPYNEPPLKAMKIRNDLPRLKHLNVSLSKGLFDRLLVRP 557
Db 1131 VMSLIGIMILEMGEPEPPYNETPTLRALYLATNGTEPKLSDYDIRFLAMCLQVDP 1190
QY 558 AORATAAEILKHPFLAKAGPASIPLMKNRTR 591
Db 1191 NKRADELHLDNFITECDVSSLSPLVKIARLK 1224

RESULT 9

T18259
serine/threonine protein kinase homolog - yeast (Candida albicans)
C/Specter: Candida albicans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18259
R/Kohler, J.R.; Pink, G.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 13223-13228, 1996
A/Title: Candida albicans strains heterozygous and homozygous for mutations in mitogen-
A/Reference number: Z11118; PMID:97075146; PMID:8917572
A/Accession: T18259
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1230 <KOH>
A/References: UNIPROT:Q92212; EMBL:U73457; NID:g1657953; PID:g1737181; PIDN:AA8388
C/Genetics:
A/Note: CST20

Query Match 27.4%; Score 846.5; DB 2; Length 1230;
Best Local Similarity 27.1%; Pred. No. 2.4e-22;
Matches 221; Conservative 114; Mismatches 220; Indels 259; Gaps 17;

QY 1 MFGKRRK-----RVEISAPSNFEHRVATGFDHOKFTGLPRQWGL 42
Db 447 MFGKNTSTSSSSSGNSHSGQEVNIKISTFNAKHLAVGIDN-GSYTGLPIEMERL 505
QY 43 I-----ESARRPPVLDPACT--TSIQCAPRTIYVSGKAGDGLTLLDPEFM 92
Db 506 LSAIGITKKEQOHPQAVMDIVAFOYDTSEN-----DDAFAKFE--HFDNN 550
QY 93 SVTRSNLSLRDSP-----PPARAENGMEEPATYARG 128
Db 551 KSSSSGMSMENTPPATPPGSSNGSGSGGAGAPSSPHRTPPSIIENKNVEQKYYTSSQM 610
QY 129 PGKAGRGPRAGHSEAGGSGDRRRAGPEKRPKS--REGSGGPOESS--RDKRPLSGPDV 185
Db 611 PRTTESK-----QSENHQPHEDNATQYTRPTFSHVQEGQFIPSRAPKRPSTPLSSMSV 665
QY 186 GTPQAPGLASGAKLAAGRPNTYPPRADTDPHSGAGCEPHD----- 226
Db 666 SHKTPSS-----QSLPRSDSQSDIRSTRPKSHQDVSPSKIKIRISISKSLKS 712
QY 227 -----VAPNGPSAGLAIPQSSSSSRPTPRAGAPSPVLAGP----- 264
Db 713 MRSKSGDKFTTHIAPRPPPSLPSIPKSKSHSASLSQLRPATNGSTTAPIPASAAFGGE 772
QY 265 -----HASEPQLAPACTPAAPAVPGPP----- 287
Db 773 NNALPKQRIINEFKAHAPR--PPPSAPRPPRPPRANULSQTSEIPQORTAPSGALA 830
QY 288 ----- 287
Db 831 DVTAPNTIYEIOQTKYQEAQOKLREKKALEBEIOLREKNERONROQETGQNNADTAG 890
QY 288 -----GPRSP-----OREPQVSHQEPRAALQOLVDDGDP 318
Db 891 GSNIAFPVPPVPPKPPSGSGGGRDAKOALLIAQKKEBKRRKQLQIIAKLKTICNRPDP 950
QY 319 SYLDNFIKIGEGSTGIVCIA-TVRSAGKLVAVKMDLRKQORRELLFNEVIMRDYOHEN 377
Db 951 ELYVDLVKIGQAGSGGVFLAHVDVRDKNIVAIKQNMLEQPKKELLINELIVKSGSSHN 1010

QY 378 VVEMVSYLVGDELAVWMEPELGGALTDIVYHTTRMNEQIAVCLAVIALSVLAAGVI 437
DB 1011 IVNFIDSTGLKGDWVIMWEGGSLTDIVHVSVEEQIGVCRFETLKGKFLHSGKVI 1070
QY 438 HRDIKSDSILTLHDSRVKLSDFGCAQVSKVPRKSLVGTFRYMAABELLRLPYGEVD 497
DB 1071 HRDIKSDNITLNMGNKITITDFGCAQINEINSKRITVGTFRYMAABEIVSKKYGPKVD 1130
QY 498 IWSIGIMVTEVNDGPPFPNEPPLKAMKIRDNLPRLKMLHKVSPSLKGFRLVLRDP 557
DB 1131 VMSIGIMITEMLBEPPLNTEPPLRALYLLATNGTPTKLKPESISYDIRKFLAMCQVDF 1190
QY 558 AQRATAAEILKGPFLAKXGPPASIVPLMRQNRTR 591
DB 1191 NKRADDELHNDNITTECDVVSLSPLVKLRK 1224

RESULT 10

S28394
probable serine/threonine-specific protein kinase (EC 2.7.1.-) STE20 - yeast (Saccharomy
N/Alternate names: protein YHL007C
C/Species: Saccharomyces cerevisiae
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
R/Accession: S28394; S46821; A47324; A57493
R/Labeler: E. J. Dignard, D. J. Hargue, D. J. Thomas, D. Y. Whiteway, M.
EMBO J. 11, 4815-4824, 1992
A/Title: The protein kinase homologous Ste20p is required to link the yeast pheromone res
A/Reference number: S28394; MUID:9309855; PMID:1464311
A/Accession: S28394
A/Molecule type: DNA
A/Residues: 1-939 <LEB>
A/Cross-references: UNIPROT:Q03497; EMBL:M94719; NID:g172746; PIDN:AAA5111.1; PID:g1727
R/Labeler: T.
submitted to the EMBL Data Library, June 1994
A/Description: The sequence of S. cerevisiae cosmid L5018.
A/Reference number: S46798
A/Accession: S46821
A/Molecule type: DNA
A/Residues: 1-939 <RAV>
A/Cross-references: EMBL:U11581; NID:g508676; PIDN:AAB69747.1; PID:g508679; MIPS:YHL007C
R/Labeler: S.W. J. Davis, R.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 452-456, 1993
A/Title: A dominant truncation allele identifies a gene, STE20, that encodes a putative
A/Reference number: A47324; MUID:93133807; PMID:8421676
A/Accession: A47324
A/Molecule type: DNA
A/Residues: 1-18, 'S', '20-133, 'M', '135-270, 'S', '272-939 <RAM>
A/Cross-references: EMBL:L04655; NID:g172585; PIDN:AAA35038.1; PID:g172586
A/Note: sequence extracted from NCI backbone (NCBI:122769, NCBI:122774)
R/Labeler: C. J. Whiteway, M. J. Thomas, D. Y. J. Leberer, E.
J. Biol. Chem. 270, 15984-15992, 1995
A/Title: Molecular characterization of Ste20p, a potential mitogen-activated protein or
A/Reference number: A57493; MUID:95332294; PMID:7608157
A/Accession: A57493
A/Status: preliminary
A/Molecule type: protein
A/Residues: 757-784 <WTA>
C/Genetics:
A/Genes: SGD:STE20
A/Cross-references: SGD:S0000999; MIPS:YHL007C
A/Map position: 8L
C/Function:
A/Description: signal transduction, required for pheromone signal transduction
C/Superfamily: protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; signal tr
F:618-871/Domain: protein kinase homology <KIN>
F:626-634/Region: protein kinase ATP-binding motif

Query Match 27 1%; Score 837; DB 2; Length 939;
Best Local Similarity 32.3%; Pred. No. 4.1e-22;
Matches 208; Conservative 98; Mismatches 191; Indels 146; Gaps 13;

QY 9 VEISAPNFEHRVHTGTFDQHQFTGLPRQMSLI EESARRPKPLVDPACITSIOPGAPK 68
DB 335 IRISTPYNAKHIIHGVDSKTEYTGLEBEMKLTLSGT 374
QY 69 TIYRSGKAGDALTLILDEFE -NNSVYTRNSLRDSDPPPARARQENGMEBPATARG 127
DB 375 -----SKREQQNMQAVMDIVAFYQDVETNG-----EDKMFXTFTT-G 414
QY 128 GPGKAGSRGRFAGHSEAGGSGDRRRAPBEKPKSREGSGGQSSSDKXPLS----- 181
DB 415 LFGS-----POVST-----PPANSFNKFPSTDSHN 441
QY 182 -GPDVGTPOPAAGLASGAKLAAGRPENTYPRADTHPSRGAQGEPPDVAPNGSAGLAIP 240
DB 442 YGSRGTGTPMSNIVMS-----PLNTDSSSANGFIFISRAPKPPSSASASAP 488
QY 241 -----QSSSSSRPPTARCAPSPGVLPAS-----BPQLAPP----- 274
DB 489 IIKSPVMSANVSPKQTHAPPTENRTSPNRSISRVA TLKKEQPLPPIPTKSTSP 548
QY 275 -----ACTPAPAVPGPPGPPQRPQSVSH-----QFRALQ 309
DB 549 IISTAHTPQVAAGSPKAPQETVTTPTSKPAQASLSKELNEKREBERRKQVAKLN 608
QY 310 LVDPGDRSYLDNFIKIGEGSTGICATVRSKGLVAVKRDLRQQRRELFNEVVI 369
DB 609 EICSDGDPSTYKALVWIKGQASGVYTAIEIGTVSAIKOMVLKQPKKELIINELV 668
QY 370 MRDVOHEVNVMSVYVGDGLAVWMEPELGGALTDIVYHTTRMNEQIAVCLAVIALS 429
DB 669 MKGSKRPIVAFIDSYLVKGDWVIMWEGGSLTDVGTCTITGQIGVCEBETLSGLE 728
QY 430 VLAQGVHNDIKSDSILTLHDSRVKLSDFGCAQVSKVPRKSLVGTFRYMAABELLRL 489
DB 729 FLHSGVTLHDIKSDNITLNMGNKITITDFGCAQINEINSKRITVGTFRYMAABEIVSR 788
QY 490 LPYGEVDIVSIGIMVTEVNDGPPFPNEPPLKAMKIRDNLPRLKMLHKVSPSLKGF 549
DB 789 KEVGPKVDIVSIGIMITEMLBEPPLNTEPPLRALYLLATNGTPTKLKPESISYDIRKFL 848
QY 550 DRLVDRPAQRATVAAELIKHPFLAK--AGPPASIVPLMRQNRTR 591
DB 849 DWICLVPEPDRASATLHDEYITTEIAEANSLSIAPLVKLRK 891

RESULT 11

T39500
serine/threonine-specific protein kinase (EC 2.7.1.-) pak1-ehk1 - fission yeast (Schizos
N/Alternate names: Ste20 homologous protein kinase 1
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
R/Accession: T39500; T45523
R/Labeler: A. J. Reinhardt, R. J. Lyne, M. J. Rajandream, M.A. J. Barrell, B. G.
submitted to the EMBL Data Library, December 1998
A/Reference number: Z21859
A/Accession: T39500
A/Molecule type: DNA
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-658 <BEC>
A/Cross-references: UNIPROT:P50527; EMBL:AL034433; PIDN:CAA22347.1; GSPDB:GN00066; SPDB:
A/Experimental source: strain 972h-, cosmid c1604
R/Marcus, S.
submitted to the EMBL Data Library, April 1997
A/Reference number: Z22999
A/Accession: T45523
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-658 <MAR>
A/Cross-references: EMBL:L41552; PIDN:AAB52609.1
C/Genetics:
A/Genes: ehk1; SPBC1604.14c
A/Map position: 1
C/Superfamily: protein kinase homology

C/Keywords: hydrolase; phosphotransferase; signal transduction

Query Match 26.7%; Score 823.5; DB 2; Length 658;

Best Local Similarity 31.5%; Pred. No. 9e-22;

Matches 189; Conservative 113; Mismatches 193; Indels 103; Gaps 12;

6 KKEVEISAPENFEHRVHTGFDQHEOKFTGLPRQMOGLI-----ESARRPKPLVDPAC 58

142 RKSTVISPDPKGVHTGVFNVDTEFTGMPTMQLALKSGITKSQVHPQAVLDAMA 201

59 ITSIGPAGKTIYVSGKAGDGLTLLDEFENMSTRNSLRDPPPARARQENMP 118

202 FYS-----QSKYLEEGA-----KPPRESTEK----- 225

119 EEPATTARAGPGKAGRGPRFAGHSEAGSGGDRRRAPPEKPKSRSGSGGQPOESSRDX 178

226 -----PLLSVALSSSSHLQPTSATSSSLYP-----SR 255

179 PLSGPDVGTPOAGLASGAKLAAGRPNTPYPRADTHPSRGAQGEPHD--VAENGPAGG 236

256 P-----APTPASSSSPLSSQTVKTTTNSARQPSPLVSSKSTDNIRSHSPV--- 305

237 LAIPQSSSSSRPPTTARAGAPSPGVLAGPASEP--QLAPPACTPAAPAVP---GPPGR 290

306 LTPPTLSTSETKHIR-----PNNSTPYQRAETSTPKKAVATQKVEAPAPR 354

291 SPQREQRVSHQ--FRALQLVVDPPDPRSYLDNFIKIGSGTGVCIATVRSGLVAV 349

355 LQKRAFRQGSNDQAVLAKQISICNPKNPFTLLRNFKIGQASGDVYSARQVGTNLSVAL 414

350 KKQDLKQQRRELLFNEVIMRDYOHENVEMVNSYLVGDELMVMEFLGALTDIVTH 409

415 KKNINQOPKKEPIVNEILVMKSHHKINIVNIDTFEYKSELMMVMEYMGSLTEVTN 474

410 TRNNEQIAVCLAVIALSVLAQGVTHRDIKSDSILLTHDGRVYKLSDFGCAQVSKV 469

475 NTLSEQIAAIKCTELTEGLHENGIVHRDIKSDNILLSDGIDICTLDFGCAQIDSNM 534

470 PRKSLVGTPTMMAPELISLTPYGPEDVMSIGIWIEMVDGPPFPNEPPLKAMKMD 529

535 TKRTTAVGTPYMAPEVYVTRKEVGFQVDSIGIMAEVGEPPYLNENPPLALVLIAT 594

530 NLPRLKMLHAKVPSLKGFLDRLVLRDPAQRATAELKHPPLAKAPPAIVPLMR 586

595 IGTPIKSRPRLSSVHFHDLFSLKSLTVNPKQRPSSGGLHHPFLKQAVPSSILPLIK 651

RESULT 12

S60170

protein kinase Pak1 - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004

C/Accession: S60170

R/Outfile: S.; Miller, P.J.; Johnson, D.I.; Creasy, C.L.; Sells, M.A.; Bagrodia, S.; For

EMO J. 14, 5908-5919, 1995

A>Title: Fission yeast pak1 (+) encodes a protein kinase that interacts with Cdc42p and

A/Reference number: S60170; PMID:96112805; PMID:8846783

A/Accession: S60170

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-658 <OTT>

A/Keywords: UNIPROT:P50527; EMBL:U22371; NID:g1122910; PIDN:AA49125.1; PID:g112

C/Superfamily: protein kinase homology

C/Keywords: ATP

F/384-637/Domain: protein kinase homology <KIN>

F/392-400/Region: protein kinase ATP-binding motif

Query Match 26.4%; Score 814.5; DB 2; Length 658;

Best Local Similarity 31.3%; Pred. No. 1.6e-21;

Matches 187; Conservative 113; Mismatches 194; Indels 103; Gaps 12;

6 KKEVEISAPENFEHRVHTGFDQHEOKFTGLPRQMOGLI-----ESARRPKPLVDPAC 58

142 RKSTVISPDPKGVHTGVFNVDTEFTGMPTMQLALKSGITKSQVHPQAVLDAMA 201

59 ITSIGPAGKTIYVSGKAGDGLTLLDEFENMSTRNSLRDPPPARARQENMP 118

202 FYS-----QSKYLEEGA-----KPPRESTEK----- 225

119 EEPATTARAGPGKAGRGPRFAGHSEAGSGGDRRRAPPEKPKSRSGSGGQPOESSRDX 178

226 -----PLLSVALSSSSHLQPTSATSSSLYP-----SR 255

179 PLSGPDVGTPOAGLASGAKLAAGRPNTPYPRADTHPSRGAQGEPHD--VAENGPAGG 236

256 P-----APTPASSSSPLSSQTVKTTTNSARQPSPLVSSKSTDNIRSHSPV--- 305

237 LAIPQSSSSSRPPTTARAGAPSPGVLAGPASEP--QLAPPACTPAAPAVP---GPPGR 290

306 LTPPTLSTSETKHIR-----PNNSTPYQRAETSTPKKAVATQKVEAPAPR 354

291 SPQREQRVSHQ--FRALQLVVDPPDPRSYLDNFIKIGSGTGVCIATVRSGLVAV 349

355 LQKRAFRQGSNDQAVLAKQISICNPKNPFTLLRNFKIGQASGDVYSARQVGTNLSVAL 414

350 KKQDLKQQRRELLFNEVIMRDYOHENVEMVNSYLVGDELMVMEFLGALTDIVTH 409

415 KKNINQOPKKEPIVNEILVMKSHHKINIVNIDTFEYKSELMMVMEYMGSLTEVTN 474

410 TRNNEQIAVCLAVIALSVLAQGVTHRDIKSDSILLTHDGRVYKLSDFGCAQVSKV 469

475 NTLSEQIAAIKCTELTEGLHENGIVHRDIKSDNILLSDGIDICTLDFGCAQIDSNM 534

470 PRKSLVGTPTMMAPELISLTPYGPEDVMSIGIWIEMVDGPPFPNEPPLKAMKMD 529

535 TKRTTAVGTPYMAPEVYVTRKEVGFQVDSIGIMAEVGEPPYLNENPPLALVLIAT 594

530 NLPRLKMLHAKVPSLKGFLDRLVLRDPAQRATAELKHPPLAKAPPAIVPLMR 586

595 IGTPIKSRPRLSSVHFHDLFSLKSLTVNPKQRPSSGGLHHPFLKQAVPSSILPLIK 651

RESULT 13

T15467

hypothetical protein C09B8.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004

C/Accession: T15467

R/Stellies, L.

submitted to the EMBL Data Library, June 1995

A/Description: The sequence of C. elegans cosmid C09B8.

A/Reference number: S61138

A/Accession: T15467

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-622 <STE>

A/Cross-references: UNIPROT:Q17850; EMBL:U29612; NID:g868273; PID:g868279; PIDN:AAA6880;

A/Experimental source: strain Bristol N2

C/Genetic: CDS: C09B8.7

A/introns: 107/1; 142/3; 192/1; 260/3; 291/3; 481/1; 505/3; 546/3; 570/3

C/Superfamily: protein kinase homology

Query Match 26.3%; Score 811.5; DB 2; Length 622;

Best Local Similarity 33.7%; Pred. No. 2.2e-21;

Matches 207; Conservative 87; Mismatches 175; Indels 145; Gaps 15;

4 KKEKVE-----ISAPNFEHRVHTGFDQHEOKFTGLPRQMOGLI-----ESARRPKP 52

109 KQKKEASEKPVISPSNFEHTIHVGDPKTSFTMPKAMARLITDSQISKQEQQNPQA 168

53 LVDPACTITSIGPAGKTIYVSGKAGDGLTLLDEFENMSTRNSLRDPPPARAR 112

169 VLD-----ALKTYTQGESGQKWLQYWMNDAPSRTPSYGLK----- 204

113 QENGMPEEPATTARAGPGKAGRGPRFAGHSEAGSGGDRRRAPPEKPKSRSGSGGQPE 172

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 10:58:31 ; Search time 199.897 Seconds

(without alignments)
1513.973 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MFGKRRKVEISAPGNFEHR.....LAKAPPAIVPLMRQNRTR 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_aprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3090	100.0	591	1	PAK4_HUMAN
2	2860	92.6	593	1	PAK4_MOUSE
3	2856	92.4	597	2	Q6ZPX0
4	2853	92.3	593	2	Q80297
5	2558	82.8	501	2	Q8N4B1
6	2202.5	71.3	438	2	Q8NDE3
7	2202.5	71.3	467	2	Q9TUS8
8	2124.5	68.8	650	2	Q90M62
9	2031	65.7	663	2	Q6CM11
10	1967	63.7	407	2	Q8K0U2
11	1748	56.6	719	2	Q8C015
12	1745	56.5	711	2	Q6NVJ4
13	1740	56.3	719	2	Q8BV80
14	1731	56.0	719	1	PAK7_HUMAN
15	1730	56.0	719	2	Q8TB93
16	1730	56.0	719	2	Q6RWS7
17	1501.5	48.6	639	1	PAK6_DROME
18	1473.5	47.7	681	1	PAK6_HUMAN
19	1464.5	47.4	558	2	Q7QGS5
20	1241	40.2	240	2	Q8NCH5
21	1160	37.5	229	2	Q9CS71
22	1096.5	35.5	540	2	Q903M1
23	1090.5	35.3	542	2	Q18637
24	948.5	30.7	704	2	Q7QD76
25	937.5	30.3	704	2	Q24190
26	937.5	30.3	704	2	Q9V113
27	936	30.3	827	2	Q61WN3
28	932.5	30.2	704	2	Q24213
29	924	29.9	544	1	PAK3_RAT
30	917	29.7	544	1	PAK3_RAT
31	907	29.4	577	2	Q803Z0

32	906.5	29.3	559	1	PAK3_MOUSE
33	905	29.3	577	2	Q6P017
34	904	29.3	524	1	PAK2_HUMAN
35	903	29.2	564	2	Q8ABX4
36	900	29.1	524	1	PAK2_RABIT
37	895	29.0	524	1	PAK2_MOUSE
38	895	29.0	524	1	PAK2_RAT
39	894	28.9	524	2	Q6TSC3
40	894	28.9	544	1	PAK1_RAT
41	892.5	28.9	545	1	PAK1_HUMAN
42	891.5	28.9	559	1	PAK3_HUMAN
43	891.5	28.9	559	1	PAK3_PANTR
44	891.5	28.9	559	1	PAK3_PONPY
45	890	28.8	517	2	Q8AW67

ALIGNMENTS

RESULT 1
ID PAK4_HUMAN STANDARD; PRT; 591 AA.
AC Q96013; Q9BU33;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated kinase 4) (PAK-4).
GN Name=PAK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Euteria; Primates; Carnivora; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99043860; PubMed=9822598; DOI=10.1093/emboj/17.22.6527;
RA Abo A., Ou J., Cammarano M.S., Dan C., Fritsch A., Band V.,
RA Bellisle B., Minden A.,
RT PAK4, a novel effector for Cdc42hs, is implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia."
RT EMBO J. 17:6527-6540(1998).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX Wehnick M.B.,
RT Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Scheffer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Discherkeno L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Boser S.A., Loewen N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Activates the JNK pathway. Implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia.

```

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
CC CDC42/p21 and weakly with RAC1.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O96013-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O96013-2; Sequence=VSP_004892; VSP_004893;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Highest expression in prostate, testis and
CC colon.
CC -1- PTM: Autophosphorylated when activated by CDC42/p21.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
CC subfamily.
CC -1- SIMILARITY: Contains 1 CRIB domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AJ011855; CA09820.1; -
CC EMBL; AF005046; AAD01210.1; -
CC EMBL; BC002921; AAH02921.1; -
CC EMBL; BC011368; AAH11368.1; -
CC EMBL; BC025282; AAH25282.1; -
CC HSP; O13153; IEFM.
CC Genew; HGNC:16059; PAK4.
CC H-InvDB; HIX0015110; -
CC MIM; 605451; -
CC GO; GO:0005794; C:Golgi apparatus; TAS.
CC GO; GO:0006928; P:signal motility; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000095; PAKbox/RhoGndg.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser Thr pkin AS.
CC InterPro; IPR002390; Ser_thr_kinase.
CC InterPro; IPR011026; MAP_C.
CC Pfam; PF00786; PBD; 1.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00285; PBD; 1.
CC SMART; SM00220; STK; 1.
CC PROSITE; PS00108; CRIB; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE NEG.
CC Alternative splicing; ATP-binding; Phosphorylation;
CC Serine/threonine-protein kinase; Transferase.
CC
CC DOMAIN 11 24 CRIB.
CC DOMAIN 25 320 linker.
CC NP_BIND 321 572 Protein kinase.
CC BINDING 327 335 ATP (By similarity).
CC ACT_SITE 350 350 ATP (By similarity).
CC ACT_SITE 440 440 Proton acceptor (By similarity).
CC VARSPIC 120 120 E->K (in isoform 2).
CC VARSPIC 121 285 /FTID=VSP_004892.
CC VARSPIC 121 285 Missing (in isoform 2).
CC SEQUENCE 591 AA; 64071 MW; 04C2A5C0B06427D5 CRC64;
SQ
Query Match 100.0%; Score 3090; DB 1; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.7e-106;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGRRKRVLSAPSNEFHRTGFDHGEQKFTGLPROMOSLIRESARRPKPLVDPACT 60
Db 1 MFGRRKRVLSAPSNEFHRTGFDHGEQKFTGLPROMOSLIRESARRPKPLVDPACT 60

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QY 61 SIOPGAPRTIVRGSGKAGDGLTLILDFENMSVTRNSLNRDSPPPARARQENGWEE 120
Db 61 SIOPGAPRTIVRGSGKAGDGLTLILDFENMSVTRNSLNRDSPPPARARQENGWEE 120
QY 121 PATTARRGGPKAGSGRFGHSEAGGSGDPRRAGPERPKSRSGSGGPGQESSDGRPL 180
Db 121 PATTARRGGPKAGSGRFGHSEAGGSGDPRRAGPERPKSRSGSGGPGQESSDGRPL 180
QY 181 SGPDPVGTGPAGLASGAKTLAAGRPENTYPRADTHPSRGAQGEPRHDVAPNGPSAGLAIP 240
Db 181 SGPDPVGTGPAGLASGAKTLAAGRPENTYPRADTHPSRGAQGEPRHDVAPNGPSAGLAIP 240
QY 241 QSSSSSSPPPRPARCAPSPGVLGPHASBPQLAPPACTPAAPVAPGPPRSPQRSPQVS 300
Db 241 QSSSSSSPPPRPARCAPSPGVLGPHASBPQLAPPACTPAAPVAPGPPRSPQRSPQVS 300
QY 301 HEOPRAALQIVVDQDDPSYLDNFTKIGESTGIVCIATVRSQKIVAKMDLRKQOR 360
Db 301 HEOPRAALQIVVDQDDPSYLDNFTKIGESTGIVCIATVRSQKIVAKMDLRKQOR 360
QY 361 ELTFNEVIMEDYGHENVMENSVLVGDELVMVMEFLGGALTDIVTHRMNEQLAAV 420
Db 361 ELTFNEVIMEDYGHENVMENSVLVGDELVMVMEFLGGALTDIVTHRMNEQLAAV 420
QY 421 CLAVLQALSTVHAAGVHRDVKSDSILLTHDGRYKLSDFGCAQVSKVPRKSLVGTPT 480
Db 421 CLAVLQALSTVHAAGVHRDVKSDSILLTHDGRYKLSDFGCAQVSKVPRKSLVGTPT 480
QY 481 WMAPELISRLLPYGPEVIMSGIWIEMVDEPPEYFNEPPLKAMKMRDNLPPPLKNLHK 540
Db 481 WMAPELISRLLPYGPEVIMSGIWIEMVDEPPEYFNEPPLKAMKMRDNLPPPLKNLHK 540
QY 541 VSPSLKGLDLRLVDRDPAQRATAELKHPFLAKAGPAPASIVPMRQNR 591
Db 541 VSPSLKGLDLRLVDRDPAQRATAELKHPFLAKAGPAPASIVPMRQNR 591

RESULT 2
PAK4 MOUSE STANDARD; PRT; 593 AA.
ID PAK4 MOUSE
AC Q8BTW9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.37) (p21-activated
DE kinase 4) (PAK-4).
GN Name=PAK4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Mikado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Choithia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard R.M., Lyons P.A.,
RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan M.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

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RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Matanabe Y., Wells C.,
RA Wuiling L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hitozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shitaki T., Maki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVE/N, TISSUE=Colon;
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield J.S.N., Krzywicki M.T., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Activates the JNK pathway. Implicated in the
CC reorganization of the actin cytoskeleton and in the formation of
CC filopodia (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
CC CDC42/p21 and weakly with RAC1 (By similarity).
CC -1- PTM: Autophosphorylated when activated by CDC42/p21 (By
CC similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STE20
CC subfamily.
CC -1- SIMILARITY: Contains 1 CRIB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, AK088512; BAC40396.1; -;
DR EMBL, BC048238; AA848238.1; -;
DR HSSP, Q13153; 1F3M.
DR MGD; MGI:1917834; Pak4.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; Pakbox/Rhodning.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR011026; WAB_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PSS0108; CRIB; 1.
DR PROSITE; PSS0107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PSS0108; PROTEIN_KINASE_ST; FALSE NEG.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 11 24 CRIB.
FT DOMAIN 25 322 Linker.
FT DOMAIN 323 574 Protein kinase.
FT NP_BIND 329 337 ATP (By similarity).
FT BINDING 352 352 ATP (By similarity).
FT ACT_SITE 442 442 Proton acceptor (By similarity).
SQ SEQUENCE 593 AA; 64622 MW; 4AFA91DD73D4C6D5 CRC64;
Query Match 92.6%; Score 2660; DB 1; Length 593;
Best Local Similarity 92.6%; Pred. No. 9.9e-98;
Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;
QY 1 MEGKKRRVEISAPSNFEHRYVTGFDQHEQKFTGLPRQWOSLIESARRPKLVDPACIT 60
DB 1 MEGKKKKRVEISAPSNFEHRYVTGFDQHEQKFTGLPRQWOSLIESARRPKLVDPACIT 60
QY 61 SIQPGAPKTYVSGKADGALTLLDDEFENNSVTRNSLRDSDPPPPARAQENGMPRE 120
DB 61 SIQPGAPKTYVSGKADGALTLLDDEFENNSVTRNSLRDSDPPPPARAQENGMPRE 120
QY 121 PATTARGGPGKSGRPFAGHSEAGGSGDRRAGREKPKSREGSGGPOSSRDKRL 180
DB 121 PATTARGGPGKSGRPFAGHSEAGGSGDRRAGREKPKSREGSGGPOSSRDKRL 180
QY 181 SGPDVGTDPAGIAGAKLAGRPNTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAP 240
DB 181 SGPDVGTDPAGIAGAKLAGRPNTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAP 240
QY 181 SGPDVGTDPAGIAGAKLAGRPNTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAP 240
DB 181 SGPDVGTDPAGIAGAKLAGRPNTYPRADTDHPSRGAQEPHDVAPNGPSAGGLAP 240
QY 241 QSSSSSSRPPTARAGPSGVGCPHASEPOLAPPA---CTPAAPAVPGPGGRSPQRE 297
DB 241 QSSSSSSRPPTARAGPSGVGCPHASEPOLAPPA---CTPAAPAVPGPGGRSPQRE 297
QY 241 QSSSSSSRPPTARAGPSGVGCPHASEPOLAPPA---CTPAAPAVPGPGGRSPQRE 297
DB 241 QSSSSSSRPPTARAGPSGVGCPHASEPOLAPPA---CTPAAPAVPGPGGRSPQRE 297
QY 298 RVSHOPFRALQVDPGPGRSYLNPFKIGSGYIVCIATVRSRSGKVAKKMDLRQ 357
DB 298 RVSHOPFRALQVDPGPGRSYLNPFKIGSGYIVCIATVRSRSGKVAKKMDLRQ 357
QY 300 RVSHOPFRALQVDPGPGRSYLNPFKIGSGYIVCIATVRSRSGKVAKKMDLRQ 359
DB 300 RVSHOPFRALQVDPGPGRSYLNPFKIGSGYIVCIATVRSRSGKVAKKMDLRQ 359
QY 358 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNNEQI 417
DB 358 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNNEQI 417
QY 360 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNNEQI 419
DB 360 QRRELLFNEVIMRDYOHENNVEMVNSYLVGDELVWMEFLGALTDIVTHRNNEQI 419
QY 418 AAVCLAVQALSVLAQGYIHRDYSSTLLTHDGRVYKLSDFGCAQVSKYPRKSLVG 477
DB 418 AAVCLAVQALSVLAQGYIHRDYSSTLLTHDGRVYKLSDFGCAQVSKYPRKSLVG 477
QY 420 AAVCLAVQALSVLAQGYIHRDYSSTLLTHDGRVYKLSDFGCAQVSKYPRKSLVG 479
DB 420 AAVCLAVQALSVLAQGYIHRDYSSTLLTHDGRVYKLSDFGCAQVSKYPRKSLVG 479
QY 478 TPYMAAPELISRLPYGPEVDIWSLGIWYTEMWDGEPYPNEPPLKAMKIRDNLPRLN 537
DB 478 TPYMAAPELISRLPYGPEVDIWSLGIWYTEMWDGEPYPNEPPLKAMKIRDNLPRLN 537
QY 480 TPYMAAPELISRLPYGPEVDIWSLGIWYTEMWDGEPYPNEPPLKAMKIRDNLPRLN 539
DB 480 TPYMAAPELISRLPYGPEVDIWSLGIWYTEMWDGEPYPNEPPLKAMKIRDNLPRLN 539
QY 538 LHKVPSLKGFLDLRLVDPDAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 591
DB 538 LHKVPSLKGFLDLRLVDPDAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 591
QY 540 LHKVPSLKGFLDLRLVDPDAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 593
DB 540 LHKVPSLKGFLDLRLVDPDAQRATAEELKHPFLAKGPPASIVPLMKQNRTR 593
RESULT 3
Q6ZFXO PRELIMINARY; PRT; 597 AA.
ID Q6ZFXO; O6ZFXO;
AC Q6ZFXO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIA1142 protein (Fragment).
GN Name=mkIA1142;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=embryonic tail;

RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hirooka S.,
 RA Suga Y., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
 RT I11, the complete nucleotide sequences of 500 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:167-180(2003).
 DR EMBL; AK129298; BAC98108.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000095; PAKbox/RhoGndg.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KM ATP-binding.
 FT NON_TER
 SQ SEQUENCE 597 AA; 64963 MW; 50C02613F77CCADA CRC64;

Query Match 92.4%; Score 2856; DB 2; Length 597;
 Best Local Similarity 92.4%; Pred. No. 1.4e-97;

Matches 549; Conservative 10; Mismatches 31; Indels 4; Gaps 2;

QY 1 MFGKRRKVEISAPSNFEHRVHTGPDQHEOKFTGLPRQWOSLIIESARRPKPLVDPACIT 60
 DB 5 MFGKRRKVEISAPSNFEHRVHTGPDQHEOKFTGLPRQWOSLIIESARRPKPLVDPACIT 64
 QY 61 SIQGAPEKTIYRSGKAGKDGALTLTLLDEFENMSTYRNSLRDSDPPPARAQENGMPEE 120
 DB 65 SIQGAPEKTIYRSGKAGKDGALTLTLLDEFENMSTYRNSLRDSDPPPARAQENGMPEE 124
 QY 121 PATTARGGPGKAGSRGFRAGSEAGSGSDRRRAGPEKRPSSRSGSGPQESRDRL 180
 DB 125 RVAPARRMAPDKAGSARATGHSSEAGSGSDRRRAGPEKRPSSRSGSGPQESRDRL 184
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
 DB 185 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 244
 QY 241 OSSSSSSRPPTRRARAPSPVGLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPPQREPO 297
 DB 245 Q-SSSSSSRPPTRRARAPSPVGLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPPQREPO 303
 QY 298 RVSHGEQFRAALQVLVDPGDPSPSYLDNFIKIGSGTGICIAVTRSSGKLVA VKMDLRKQ 357
 DB 304 RVSHGEQFRAALQVLVDPGDPSPSYLDNFIKIGSGTGICIAVTRSSGKLVA VKMDLRKQ 363
 QY 358 QRRELLFNEVIMRDYOHENYVEMTNSYLVDDELAVVNEFLEGALTDIVHTHNNBEOI 417
 DB 364 QRRELLFNEVIMRDYOHENYVEMTNSYLVDDELAVVNEFLEGALTDIVHTHNNBEOI 423
 QY 418 AAVCLAVTQALSYLHAQGVTHRDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVG 477
 DB 424 AAVCLAVTQALSYLHAQGVTHRDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVG 483
 QY 478 TTPYMAPELISRLPGPEVDIMSLGIMVTEWVDEGPPYFNBPPLKAMMITEIDNLPRLKN 537
 DB 484 TTPYMAPELISRLPGPEVDIMSLGIMVTEWVDEGPPYFNBPPLKAMMITEIDNLPRLKN 543
 QY 538 LHKVSPSLKGFIDRLVDPQORATPAELKHGFLAKAGPPASIVPLMRQNRTR 591

DB 544 LHKVSPSLKGFIDRLVDPQORATPAELKHGFLAKAGPPASIVPLMRQNRTR 597

RESULT 4
 ID Q80297 PRELIMINARY; PRT; 593 AA.
 AC Q80297;
 DT 01-UTN-2003 (TrEMBLrel. 24, Created)
 DT 01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE P21-activated protein kinase 4.
 GN Name=Pak4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=22526742; PubMed=12529371; DOI=10.1074/jbc.M205875200;
 RA Lu Y., Pan Z.Z., Devaux Y., Ray P.;
 RT "p21-activated protein kinase 4 (PAK4) interacts with the keratinocyte
 RT growth factor receptor and participates in keratinocyte growth factor-
 RT mediated inhibition of oxidant-induced cell death.";
 RL J. Biol. Chem. 278:10374-10380(2003).
 DR EMBL; AY217016; AAC61496.1; -;
 DR HSBP; Q13153; IFSW.
 DR MGD; MGI:1917834; Pak4.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000095; PAKbox/RhoGndg.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR01026; MASP_C.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KM ATP-binding; Kinase.
 FT NON_TER
 SQ SEQUENCE 593 AA; 64666 MW; D7B3BD36706B4AF4 CRC64;

Query Match 92.3%; Score 2853; DB 2; Length 593;
 Best Local Similarity 92.6%; Pred. No. 1.8e-97;

Matches 550; Conservative 9; Mismatches 31; Indels 4; Gaps 2;

QY 1 MFGKRRKVEISAPSNFEHRVHTGPDQHEOKFTGLPRQWOSLIIESARRPKPLVDPACIT 60
 DB 1 MFGKRRKVEISAPSNFEHRVHTGPDQHEOKFTGLPRQWOSLIIESARRPKPLVDPACIT 60
 QY 61 SIQGAPEKTIYRSGKAGKDGALTLTLLDEFENMSTYRNSLRDSDPPPARAQENGMPEE 120
 DB 61 SIQGAPEKTIYRSGKAGKDGALTLTLLDEFENMSTYRNSLRDSDPPPARAQENGMPEE 120
 QY 121 PATTARGGPGKAGSRGFRAGSEAGSGSDRRRAGPEKRPSSRSGSGPQESRDRL 180
 DB 121 PATTARGGPGKAGSRGFRAGSEAGSGSDRRRAGPEKRPSSRSGSGPQESRDRL 180
 QY 181 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
 DB 181 SGPDVGTTPQAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGLAIP 240
 QY 241 OSSSSSSRPPTRRARAPSPVGLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPPQREPO 297
 DB 241 Q-SSSSSSRPPTRRARAPSPVGLGPHASEPOLAPPA---CTPAAPAVGPPGPPRSPPQREPO 299
 QY 298 RVSHGEQFRAALQVLVDPGDPSPSYLDNFIKIGSGTGICIAVTRSSGKLVA VKMDLRKQ 357

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DB 300 RVSHQFRAALQVDPGDSRLDIFIKIGSGTSIVCIATVRSSSGKIIVAVKMDLRKQ 359
QY 358 QRRLLFNFVIMRDQCHENVEMNSYVGDLMVWMEFLRGALTDIVTTRMNEEOI 417
DB 360 QRRLLFNFVIMRDQCHENVEMNSYVGDLMVWMEFLRGALTDIVTTRMNEEOI 419
QY 418 AAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSEKVPKRSVLG 477
DB 420 AAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSEKVPKRSVLG 479
QY 478 TTYMNAPELISRLPYGPEVDIWSLGIWVTEWYDGEPPYNEPPLKAMKXIRDNLPRLKX 537
DB 480 TTYMNAPELISRLPYGPEVDIWSLGIWVTEWYDGEPPYNEPPLKAMKXIRDNLPRLKX 539
QY 538 LHKVPSLKGFLDRLVDPAPQATPAELIKHPFLAKAGPPASIVPLMKQNRTR 591
DB 540 LHKVPSLKGFLDRLVDPAPQATPAELIKHPFLAKAGPPASIVPLMKQNRTR 593

RESULT 5
Q8N4E1 PRELIMINARY; PRT; 501 AA.
AC Q8N4E1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PAK4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Plange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DB EMBL: BC034511; ANH34511.1; -
DB HSPF: Q13153; 1F3M.
DB GO: GO:0005524; F:ATP binding; IEA.
DB GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DB GO: GO:0004648; F:protein amino acid phosphorylation; IEA.
DB InterPro: IPR011009; Kinase like.
DB InterPro: IPR000985; PAKbox/Rhoindng.
DB InterPro: IPR000719; Prot_kinase.
DB InterPro: IPR002290; Ser_thr_kinase.
DB InterPro: IPR011026; WASP_C.
DB Pfam: PF00786; PBD; 1.
DB Pfam: PF00069; Pkinase; 1.

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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PSS0108; CRIB; 1.
DR PROSITE; PSS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding.
SQ SEQUENCE 501 AA; 54940 MW; 6E86240CE65E79D CRC64;

Query Match      82.8%; Score 2558; DB 2; Length 501;
Best Local Similarity 84.8%; Pred. No. le-86;
Matches 501; Conservative 0; Mismatches 0; Indels 90; Gaps 1;

QY 1 MFGKKRKRVEISAPSNFHRVHTGFDQHEQKFTGLPRQWQSILIESARRPKPLVDPACTT 60
DB 1 MFGKKRKRVEISAPSNFHRVHTGFDQHEQKFTGLPRQWQSILIESARRPKPLVDPACTT 60
QY 61 SIQPGAPKTIIVGSKAKDGLTLLDEFENNSVTRSNLRDSDPPPPARAOENGMPEE 120
DB 61 SIQPGAPKTIIVGSKAKDGLTLLDEFENNSVTRSNLRDSDPPPPARAOENGMPEE 120
QY 121 PATTARGGPGKAGSKGRFAGHSEAGSGSDRRRAGEKPKSRBSGGPQESSRDKRL 180
DB 121 PATTARGGPGK-----
QY 181 SGPDVQTQPGAGLASGAKLAAGRFPNTYPRADTDHPSRGAQGEPHDVAENGSAGLAIP 240
DB 181 SGPDVQTQPGAGLASGAKLAAGRFPNTYPRADTDHPSRGAQGEPHDVAENGSAGLAIP 240
QY 132 -----
DB 132 -----
QY 241 QSSSSSRPPTARAGAPSPGVIGPHASEPOLAPACTPAAPVPGPGRSPQREPORVS 300
DB 151 QSSSSSRPPTARAGAPSPGVIGPHASEPOLAPACTPAAPVPGPGRSPQREPORVS 210
QY 301 HQGFRAALQVDPGDSRLDIFIKIGSGTSIVCIATVRSSSGKIIVAVKMDLRKQNR 360
DB 211 HQGFRAALQVDPGDSRLDIFIKIGSGTSIVCIATVRSSSGKIIVAVKMDLRKQNR 270
QY 361 ELLFNFVIMRDQCHENVEMNSYVGDLMVWMEFLRGALTDIVTTRMNEEOIAV 420
DB 271 ELLFNFVIMRDQCHENVEMNSYVGDLMVWMEFLRGALTDIVTTRMNEEOIAV 330
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSEKVPKRSVLGTPY 480
DB 331 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSEKVPKRSVLGTPY 390
QY 481 WNAPELISRLPYGPEVDIWSLGIWVTEWYDGEPPYNEPPLKAMKXIRDNLPRLKX 540
DB 391 WNAPELISRLPYGPEVDIWSLGIWVTEWYDGEPPYNEPPLKAMKXIRDNLPRLKX 450
QY 541 VSPSLKGFLDRLVDPAPQATPAELIKHPFLAKAGPPASIVPLMKQNRTR 591
DB 451 VSPSLKGFLDRLVDPAPQATPAELIKHPFLAKAGPPASIVPLMKQNRTR 501

RESULT 6
Q8NDE3 PRELIMINARY; PRT; 438 AA.
AC Q8NDE3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp547G182.
GN Name=DKFZp547G182;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;

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RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL834236; CAD38914.2; -;
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004674; P:protein amino acid phosphorylation; IEA.
 DR ATP-binding; Hypothetical protein.
 SQ SEQUENCE 438 AA; 48267 MW; 4A56E8BC9883 CRC64;

Query Match 71.3%; Score 2202.5; DB 2; Length 438;
 Best Local Similarity 74.1%; Pred. No. 9.4e-74;
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;

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QY 1 MFGKKKKVEISAPNFEHRYVHTGFDQHEQKFTGLPRQWQSLIESARPKLVDPACIT 60
DB 1 MFGKKKKVEISAPNFEHRYVHTGFDQHEQKFTGLPRQWQSLIESARPKLVDPACIT 60
QY 61 SIQPGAPK----- 68
DB 61 SIQPGAPK----- 68
QY 121 PATTARGGPGKAGSGRFRAGHSEAGGSGDRRRAPGPKSRGSGGPOESSRDKRPL 180
DB 69 ----- 68
QY 181 SGPDVGTQPPAGLASGAKLAAGRPPNTYPRADTHPSRGAQGEPRHVAVNGPSAGLAIP 240
DB 69 ----- 87
QY 241 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGSRSPQREPORVS 300
DB 88 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGSRSPQREPORVS 147
QY 301 HEQFPAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 360
DB 148 HEQFPAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 207
QY 361 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIDIVHTHNEEQIAAV 420
DB 208 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIDIVHTHNEEQIAAV 267
QY 421 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVXLSDFGCAQVSKVEPRKSLVGTPT 480
DB 268 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVXLSDFGCAQVSKVEPRKSLVGTPT 327
QY 481 WMAPELISRLPYGPEVDIWSIGIWIEMVDGEPFNEPPLKAMKIMRDNLPRLKXNLHK 540
DB 328 WMAPELISRLPYGPEVDIWSIGIWIEMVDGEPFNEPPLKAMKIMRDNLPRLKXNLHK 387
QY 541 VSPSLKGFIDRLVDRDPAQRATTAELKHPFLAKAGPPASIVPLMRQNRTR 591
DB 388 VSPSLKGFIDRLVDRDPAQRATTAELKHPFLAKAGPPASIVPLMRQNRTR 438

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RESULT 7

Q9ULS8 PRELIMINARY; PRT; 467 AA.

AC Q9ULS8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE KIAA1142 protein (Fragment).
 GN Name=KIAA1142;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20039618; PubMed=10574461;
 RA Hikosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
 RT "Characterization of cDNA clones selected by the Genemart analysis
 from size-fractionated cDNA libraries from human brain.";

RL DNA Ref. 6:329-336(1999).
 DR EMBL: AB032968; BAA86456.1; -;
 DR HSSP: Q13153; 1F3M.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004674; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000095; PAKbox/Rho-binding.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR002290; Ser. Thr. kinase.
 DR InterPro: IPR011026; WASP_C.
 DR Pfam: PF00786; PBD; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot. kinase; 1.
 DR SMART: SMO0285; PBD; 1.
 DR SMART: SMO0220; S_TKC; 1.
 DR PROSITE: PS50108; CRIB; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding.
 FT NON TER 1
 SQ SEQUENCE 467 AA; 51464 MW; EC342B8F5C5E3940 CRC64;

Query Match 71.3%; Score 2202.5; DB 2; Length 467;
 Best Local Similarity 74.1%; Pred. No. 9.9e-74;
 Matches 438; Conservative 0; Mismatches 0; Indels 153; Gaps 1;

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QY 1 MFGKKKKVEISAPNFEHRYVHTGFDQHEQKFTGLPRQWQSLIESARPKLVDPACIT 60
DB 30 MFGKKKKVEISAPNFEHRYVHTGFDQHEQKFTGLPRQWQSLIESARPKLVDPACIT 89
QY 61 SIQPGAPK----- 97
DB 90 SIQPGAPK----- 97
QY 121 PATTARGGPGKAGSGRFRAGHSEAGGSGDRRRAPGPKSRGSGGPOESSRDKRPL 180
DB 98 ----- 97
QY 181 SGPDVGTQPPAGLASGAKLAAGRPPNTYPRADTHPSRGAQGEPRHVAVNGPSAGLAIP 240
DB 98 ----- 116
QY 241 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGSRSPQREPORVS 300
DB 117 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGSRSPQREPORVS 176
QY 301 HEQFPAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 360
DB 177 HEQFPAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLKKQQR 236
QY 361 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIDIVHTHNEEQIAAV 420
DB 237 ELLFNEVIMRDYQHENVEMTNSYLVDGLVWMEFLGGLTIDIVHTHNEEQIAAV 296
QY 421 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVXLSDFGCAQVSKVEPRKSLVGTPT 480
DB 297 CLAVIALSVLHAQGVHHRDIKSDSILLTHDGRVXLSDFGCAQVSKVEPRKSLVGTPT 356
QY 481 WMAPELISRLPYGPEVDIWSIGIWIEMVDGEPFNEPPLKAMKIMRDNLPRLKXNLHK 540
DB 357 WMAPELISRLPYGPEVDIWSIGIWIEMVDGEPFNEPPLKAMKIMRDNLPRLKXNLHK 416
QY 541 VSPSLKGFIDRLVDRDPAQRATTAELKHPFLAKAGPPASIVPLMRQNRTR 591
DB 417 VSPSLKGFIDRLVDRDPAQRATTAELKHPFLAKAGPPASIVPLMRQNRTR 467

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RESULT 8

Q90W62 PRELIMINARY; PRT; 650 AA.

AC Q90W62;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE PAKS protein.
 GN Name=PAKS;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBITaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stage VI oocyte;
 RA Cau J., Faure S., Delaert C., Morin N.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ277826; CAC40979.1; -.
 DR HSSP: Q13153; 1F3M.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004668; F:protein amino acid phosphorylation; IEA.
 DR Pfam: PF00786; PBD; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00285; PBD; 1.
 DR PROSITE: PS50108; CRIB; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding.
 SQ SEQUENCE 650 AA; 73736 MW; 927AD6C6ACD4A081 CRC64;
 Query Match 68.8%; Score 2124.5; DB 2; Length 650;
 Best Local Similarity 66.4%; Pred. No. 9.5e-7; Indels 91; Gaps 13;
 Matches 442; Conservative 43; Mismatches 90;
 QY 1 MFGKRRKRYEISAPNFHRVHTGPDHGEQKFTGLPRWQSLIEESARPKPLVDPACT 60
 DB 1 MFAKKKRRVEISAPNFHRVHTGPDHGEQKFTGLPRWQSLIEESARPKPLVDPACT 60
 QY 61 STPGAPKTIIVRGSKAKGALTLILDEFENNSVTSNSLRDSP--PPPARQENGW 117
 DB 61 TTKHVPQKTIIVGNKMSLDGSLAMLDEFDMVCSNSLRRESPPCQPEGRFHONGW 120
 QY 118 PE-----EPAITLRG----- 128
 DB 121 SEWRVQQRREDGSGERNNRSEHRRERQREHRAVPPQPRGQSPNKHPPPPDYKCI 180
 QY 129 PGKAGSRGPFAGHSEAG-----GSGD-----RRAGPEKPKS--REGSGAPQ 172
 DB 181 PEKRGPR-----SHEKSGREYVGNDRGHSDPYERVVKDKGEEKPKKAYTSGEGSPQ 235
 QY 173 SSRDRKPLSGPDVGTQPAAGLASGAY-LAAGRPNTYPPRADTHPSRGAQGEPHDVA PNG 231
 DB 236 SPRDRKPLSGPNIRTRGSSSTGSDGVVQTETGRFPNTYPPRAETD-PRGGAHQVSDRSRTV 294
 QY 232 P-----SAGGLAIPSSSSSSSPPRRAGAPRGVLGPAASRPLAPACTPAARAVNG 285
 DB 295 PLDSKSSVSKSGSRPPQGGVKKPPEK-----PHTQLAPHSPPQSLSRPQT-----QH 344
 QY 286 PPGPRSPQEPQVSHQFRAALQLVDDPPRSYLDNFIKIGEGTGIVCIATVSSSG 345
 DB 345 PPGPRSPQEPQVSHQFRAALQLVDDPPRTYLDNFIKIGEGTGIVCIATVSSSG 404
 QY 346 LVAVKKMDLRKQGRRELLFNEVVIKRDYQHENVEMVNSYLVGDELAVNMELEGALTD 405
 DB 405 LVAVKKMDLRKQGRRELLFNEVVIKRDYQHENVEMVNSYLVGDELAVNMELEGALTD 464
 QY 406 IYHTHMEHQTAACVLAVYALSYVAAGVTHRDIKSSILLTHGRVYLSFGCAQY 465
 DB 465 IYHTHMEHQTAACVLAVYALSYVAAGVTHRDIKSSILLTHGRVYLSFGCAQY 524
 QY 466 SKEVPRKSLVGTPTVMAPELLIRLPYGEVDIWSIGIMVEMVDEPPYFNEPPLKAK 525
 DB 525 NKEVPRKSLVGTPTVMAPELLIRLPYGEVDIWSIGIMVEMVDEPPYFNEPPLKAK 564

QY 526 MTRDNLPRRLKNIHKVSPSLKGFILDRILVDDPAORATABLKHPPIAKAGPPASTVPLM 565
 DB 585 MTRDNLPRRLKNIHKVSPSLKGFILDRILVDDPAORATABLKHPPIAKAGPPASTVPLM 644
 QY 586 RQNRTR 591
 DB 645 RQNRTR 650
 RESULT 9
 ID 06GM11 PRELIMINARY; PRT; 663 AA.
 AC 06GM11;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 DE 29c:92014.
 GN ORFNames=zgc:92014;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBITaxID=7955;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Fellngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caesvant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettleman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC074067; AAH74067.1; -.
 DR ZFIN: ZDB-GENE-040704-69; zgc:92014.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004668; F:protein tyrosine kinase activity; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR InterPro: IPR011026; Kinase like.
 DR InterPro: IPR000095; PAKbox/Rhodning.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR011026; WASF_C.
 DR Pfam: PF00786; PBD; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00285; PBD; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS50108; CRIB; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; P850011; PROTEIN_KINASE_DOM; 1.
KM ATP-binding.
SQ SEQUENCE 663 AA; 74760 MM; 61FB6F87BE40550 CRC64;
Query Match 65.7%; Score 2031; DB 2; Length 663;
Best Local Similarity 62.0%; Pred. No. 2,6e-67;
Matches 427; Conservative 50; Mismatches 88; Indels 124; Gaps 16;
QY 1 MGKKRK-RVELISAPNFEHRYHTGPDQHEOKFTGLPRWQSLIESSARPRPLVDPAKI 59
DB 1 MFSKKKKRIQISAPNFEHRYHTGPDQHEOKFTGLPRWQSLIESSARPRPLVDPAKI 60
QY 60 TSIQGPARTIVRGSGKADGALTLLDDEFEMNSVTRSNLSLRDSPP----- 106
DB 61 TTVERP--RTIYRGKIGDGSITWLLDDEFMTSVTRSNLSLRGSPPLQPRSDSGSGGH 118
QY 107 -----PPARAQENGMPEEPATTAAG-- 127
DB 119 ENGEPHYVHTDYGSGKERKPRQEPHTDPRQSGPGRSSREDGRPQQ--QPRGQEP 175
QY 128 -----GPGKAGSR-----FAGHSEAGGSGSDRRRAQEPKPKSSREGSGP 170
DB 176 SHHKERDWTTPGQHRERDRERERPRDYSDHV-----REGANDKKPKSSYTGROSS 228
QY 171 QESSRDKRLSPGPDVGTPO---PAGLASGAKLAAGRPFNTYPRADT-----HPS 217
DB 229 PGRPRKRLSPGPNRTPLPTVEGYTKAQ-QTGRPFNTYRSBSDSGRTPSGQDLKPA 287
QY 218 KRAQGEPRDVAIVNGPSAGGLAIPOSSSSSRPRTRARGAPSGVLGPHASEPO--LAPPA 275
DB 288 KSHSTYH---NGPSAG--PYRGSGSSSSS-----GGQTSQSGPHRSEPHASHPA 334
QY 276 CTPAAP--AVGPPRP-----RSRPRQPVSHSEORRALQIVVDDGDPSPSYD 322
DB 335 LQEPHPGMPPPPPKPSGPGAPDSQTRKPRKPKVSHQPRALQIVVDDGDPSPSYD 394
QY 332 NFIKIGESTGIVCIATVYRSGKLVAVKMDLRKQRRRLTFNEVIMRDOYHEVENVY 382
DB 395 HIYKIGESTGIVCIATVYTKGLVAVKMDLRKQRRRLTFNEVIMRDOYHEVENVY 454
QY 383 NSYLVGDELMVMELEGALTDIVTHTRMNEBOIAVCLAVLQALSVLAAGSVTHRDIK 442
DB 455 NSYLVGDELMVMELEGALTDIVTHTRMNEBOISTVCLSVLAKLSVHSGVTHRDIK 514
QY 443 SSIILTHDGRVYKLSDFGCAOVSKVPRKSLVNGPYMAABELLSRLPYGSEVDIWSFG 502
DB 515 SSIILTHDGRVYKLSDFGCAOVSKVPRKSLVNGPYMAABELLSRLPYGSEVDIWSFG 574
QY 503 INVIEKVDGPPYFNEPPLKAMKMTKMDNLPRLKKNLHKVSPSLKGFRLDLVYRDPQORAT 562
DB 575 INVIEKVDGPPYFNEPPLKAMKMTKMDNLPRLKKNLHKVSPSLKGFRLDLVYRDPQORAT 634
QY 563 AAELLKHPFLAKAGPPASIVPLMRQNRTR 591
DB 635 AOELLKHPFLAKAGPPASIVPLMRQNRTR 663
RESULT 10
Q8K0U2 PRELIMINARY; PRT; 407 AA.
ID Q8K0U2
AC Q8K0U2
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Pak4 protein (fragment).
GN Name=Pak4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.,
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC030389; AAH0389.1; -.
DR HSP, Q13153; I53M.
DR MGD; MG1:1917834; Pak4.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot. Kinase.
DR InterPro; IPR02290; Ser Thr kinase.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot. Kinase; 1.
DR SMART; SM00220; S TKC; 1.
DR PROSITE; P800107; PKINASE_ATP; 1.
DR PROSITE; P850011; PROTEIN_KINASE_DOM; 1.
KM ATP-binding.
KW NON TER
SQ SEQUENCE 407 AA; 44339 MM; 921689734DF9D710 CRC64;
Query Match 63.7%; Score 1967; DB 2; Length 407;
Best Local Similarity 94.5%; Pred. No. 3.8e-65;
Matches 380; Conservative 5; Mismatches 13; Indels 4; Gaps 2;
QY 193 LASGAKLAGRPFTYPRADTDHPSRGAQGEPRDVAIVNGPSAGGLAIPOSSSSSRPPTR 252
DB 7 LITGKLAAGRPFTYPRADTDHPSRGAQGEPRDVAIVNGPSAGGLAIPOSSSSSRPPTR 65
QY 253 ARGAPSPVLCPHASEPOLAPPA--CTPAAPAVGPPGPPSPQREPRQVSHQPRALQ 309
DB 66 ARGAPSPVLCPHASEPOLAPPA--CTPAAPAVGPPGPPSPQREPRQVSHQPRALQ 125
QY 310 LVNPDGPRSYLDNPTIKIGESTGIVCIATYRSGKLVAVKMDLRKQRRRLTFNEVY 369
DB 126 LVNPDGPRSYLDNPTIKIGESTGIVCIATYRSGKLVAVKMDLRKQRRRLTFNEVY 185
QY 370 MEDYQHEVNVMEVSYLVGDELMVMELEGALTDIVTHTRMNEBOIAVCLAVLQALS 429
DB 186 MEDYQHEVNVMEVSYLVGDELMVMELEGALTDIVTHTRMNEBOIAVCLAVLQALS 245
QY 246 VLAHQGVTHRDIKSDSILTHDGRVYKLSDFGCAOVSKVPRKSLVNGPYMAABELISR 305
DB 430 VLAHQGVTHRDIKSDSILTHDGRVYKLSDFGCAOVSKVPRKSLVNGPYMAABELISR 489
QY 430 VLAHQGVTHRDIKSDSILTHDGRVYKLSDFGCAOVSKVPRKSLVNGPYMAABELISR 489
DB 246 VLAHQGVTHRDIKSDSILTHDGRVYKLSDFGCAOVSKVPRKSLVNGPYMAABELISR 305
QY 490 LPYGEVDIWSFGVAVVEMVNGGPPYFNEPPLKAMKMTKMDNLPRLKKNLHKVSPSLKGF 549
DB 306 LPYGEVDIWSFGVAVVEMVNGGPPYFNEPPLKAMKMTKMDNLPRLKKNLHKVSPSLKGF 365
QY 550 DRLVYRDPQORATAAELLKHPFLAKAGPPASIVPLMRQNRTR 591

366 DRLLVNDPAQRATPAELHGHPELITKAGPASTVPLMRQHRTR 407

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RESULT 11
ID      08C015      PRELIMINARY;      PRT;      719 AA.
AC      08C015;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE      enriched library, clone#430627N20 product:SERINE/THREONINE-PROTEIN
DE      KINASE PAK 5 (EC 2.7.1.1-) (P21-ACTIVATED KINASE 5) (PAK-5)
DE      homolog.
GN      Mus musculus (Mouse).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX      MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA      Carninci P., Hayashizaki Y.,
RL      "High-efficiency full-length cDNA cloning.",
RL      Meth. Enzymol. 303:19-44(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX      MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA      RIKEN FANTOM Consortium;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA      the FANTOM Consortium;
RT      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX      MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA      Carninci P., Shibata K., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
RA      Konno H., Ozaki Y., Muramatsu M., Hayashizaki Y.,
RT      "Normalization and subraction of cap-trapper-selected cDNAs to
RT      prepare full-length cDNA libraries for rapid discovery of new genes.";
RL      Genome Res. 10:1617-1630(2000).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX      MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA      Konno H., Akiyama J., Nishi K., Kitsumai T., Teshiro H., Itoh M.,
RA      Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA      Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kasaiyagi K.,
RA      Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA      Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawaki J.,
RA      Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT      "RIKEN integrated sequence analysis (RISA) system-384-format
RT      sequencing pipeline with 384 multicapillary sequencer.";
RL      Genome Res. 10:11757-1771(2000).
RN      [6]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA      Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA      Fukuda S., Furuno M., Hanagata T., Hara A., Hashizume W.,
RA      Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA      Hori F., Imcanti K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA      Katoh H., Kawai Y., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
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RA Kurihara O., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Mishi K., Nomura K., Numazaki R., Onno M., Ohashi N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Saegaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Kahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK032593; BAC7939.1; -.
DR HSSP; Q13153; 1F3M.
DR MGD; MGI:1920334; Pak7.
DR GO; GO:0005573; C:mitochondrion; IDA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR InterPro; IPR011009; Kinase_lke.
DR InterPro; IPR000095; Pakbox/RhoGndg.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Fhr_kinase.
DR InterPro; IPR011026; WASP_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding, Kinase.
SQ SEQUENCE 719 AA; 80948 MW; 5E16D2318C328CD CRC64;

	Query Match	56.6%;	Score 1748;	DB 2;	Length 719;	
	Best Local Similarity	52.9%;	Pred. No. 6.4e-57;			
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Qy	1 MFGRRKRKVEISAPSEFHRVHTGFPDHOEKFTGLPRQWOSLIESARRPRLVDPACT	60				
Dd	1 MFGRKKKIRISGPSNFHRVHTGFDPQEQFTGLPQQMHSLLADTANRKPMDVCIT	60				
Qy	61 SIQPGAKTIYRGSKAKDGALTLTLDDEFEMSTSTRNSLRDSPPPP--AAAR----	112				
Dd	61 PIQLAPMKTIVRGKSGCKETSINGLLDFDNISTVRNSLSRKESPPTPDGAASRIQSHS	120				
Qy	113 QENGM-----PEEPATTAGCPKPKASSRFA-----GH-----	141				
Dd	121 EENGFIFFSQYSSSDTTADYTTEKYDRSLGYGDLDYYKSSHAAQNGAMOMKGDA	180				
Qy	142 -----SBAGSGSGDDRRA-----	154				
Dd	181 YYPEMKSLKTDLAGFVDVYHTHLDSLKSSEBYCGLRWIDYORASSSPFLDYSFOLTPSKTA	240				
Qy	155 -----GP-----EKPQRSBESSGGPOSSNRKRPLSGDVOTP-QPA 191					
Dd	241 GTSRCSKESLAYSESMDGFLDDYDRRPKSSYLHQTSPOPAMR-QRSKSGGLEBPMPMF	299				
Dd	192 GLASGAKTLAARGPNTY-----BRADTDH-----PSRGAQGEPHDVDANCP	232				
Dd	300 GASAFKHHPHGHSNASTYTRLSPTMCIRKVODRAQMVPSPPLSS-----DTYRGPF	354				
Qy	233 SAGGLAIPOS-----SSSSRPPTARKG-----PSPGVLGPASEPQLAAPRCTPAAP	281				
Dd	355 T----KLPOQSOKAGVSSGSHOYPGSYGHNKASLYHHNPILQTSQVITSAYVL-SGLSISSS	409				
Qy	282 AVPCPPCRSPORPORPVSHOEOPRALQVLVDPGDPSPSYLDNFKIGEGSGIYCIAIVR	341				
Dd	410 TYPPBSMGSSSDQPSRVSHQEOPRALQVLVSPDPREYLDNFKIGEGSGIYCIAITEK	469				
Qy	342 SSGLVAVKKMDLRKQQRRELFNEVVIMEDYOHENVTVMNSTLVGDELMVMEFLIEGG	401				
Dd	470 HTGQAVAVKKMDLRKQQRRELLENEVVIMEDYHNDNVDMNSTLVGDELMMVMEFLIEGG	529				
Qy	402 ALTDIVYHTMNEBOILAACLVALQALSYLAACGVNHRDKSNSTLLTHGGRVCLSPRGF	461				
Dd	530 ALTDIVYHTMNEBOILAACLVALSYLKALSYLANCGVNHRDKSNSTLLTSQRIKLSPRGF	589				

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RN Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RN Kono H., Akiyama J., Nishi K., Kitsuai T., Taenilo H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX Adachi J., Aizawa K., Akimura T., Aizawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraga T., Hirozane T.,
RA Hori F., Imetani K., Ishii Y., Itoh M., Kageura I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takaishi F., Takeki-Akhiba S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL AK079080; BAC37528.1; -.
DR HSSP; Q3153; 1F3M.
DR MGD; MGI:1920334; Pak7.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO; GO:0006166; P:anti-apoptosis; IDA.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR000095; PAKbox/Rhodning.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR011026; WASP_C.

DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS0108; CRIB; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR KATP-binding; Kinase.
SQ SEQUENCE 719 AA; 80967 MW; F1E33DCB8C39875B CRC64;
Query Match 56.3%; Score 1740; DB 2; Length 719;
Best Local Similarity 52.7%; Pred. No. 1,3e-56;
Matches 384; Conservative 65; Mismatches 129; Indels 150; Gaps 16;
QY 1 MFGKRRKRVISAPNSFEHRYHTGPDQHEQKFTGLPRQMSLIIESARRPKLVDPACTT 60
DB 1 MFGKRRKRVISAPNSFEHRYHTGPDQHEQKFTGLPRQMSLIIESARRPKLVDPACTT 60
QY 61 STPGAPKTIYRGSKAKDGLTLTLDPEFMSVYRSNLRDSDPP-----RAR----- 112
DB 61 STPGAPKTIYRGSKAKDGLTLTLDPEFMSVYRSNLRDSDPP-----RAR----- 112
QY 113 QENGM-----PEEPATARGGPGKASGRPA-----GH----- 141
DB 121 EENGFITPSQYSESDTTADYTTKRYDSLYGDDLDLYKSHAKONGHAMKMGDA 180
QY 142 -----SEAGSGSGDRRA----- 154
DB 181 YYPEMKSILKTDLAFVVDYHTLDSLRKSEYGDLRWDYQRASSSPDLYSFQLTFSPTA 240
QY 155 -----GR-----EKRPKSSREGSGPPESRRDRPLSGPVGTP-QQA 191
DB 241 GTSRCKESLAVSESDWGSPLDDYDRPKSSYLQTSPPQAMV-QKSKSGSGIQEPMMP 299
QY 192 GLASGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEPPHDVAPNGP 232
DB 300 GASAPFTHQGSHSYSTYPRLSSEPTMCIPKDYDRAQVVPSPPLSGS-----DYTRPDP 354
QY 233 SAAGLAIPQS-----SSSSSRPPTRARGA-----PSPGVLPNASEPQLAPACTPAAP 281
DB 355 T-----KLPGOSKAGYSSGSHQYPSGYNHKAISLYNHPSLQTSQYISTASYL-SSLSISS 408
QY 282 AVDPGPPSPSPREPRQVHEQPRALQVYDPPGPRSLYDNPFIKIGESTGIVCAATVR 341
DB 410 TYPPSPGWSSSQOQPSRVSHQFRALQVSPGPREFLDNFIKIGESTGIVCAATEK 469
QY 342 SSGKLVAVKMDLRKQQRRELLFNEVIMRDYQHENVVEYNSYLVGDELMVMEFLREG 401
DB 470 HTGQVAVAKMDLRKQQRRELLFNEVIMRDYHHDVNDVMTNSYLVGDELMVMEFLREG 529
QY 402 ALTDIVTTRNMEBOIAVCAVLQALSYLAQGVIRDKSDSILLTHDGRVKLSDFGR 461
DB 530 ALTDIVTTRNMEBOIAVCAVCLSYLAKSLYLNHGVYIHRDKSDSILLTSDGRKLSDFGR 589
QY 462 CAQVSKVPRRSYLVGTPTWMAPELISRLPYEPEDVINSLGIMVEMVDGEPYFPEPL 521
DB 590 CAQVSKVPRRSYLVGTPTWMAPEVLSRLPYEGTEVDIMSLGIMVEMVDGEPYFPEPL 649
QY 522 KMKMIRNDLPRLKNIHKVSPSLKGFPLRLVDPDAQATAAELKKPFLAKAGAPASI 581
DB 650 QAMRRIRDSLPRAVKDILHKVSMKRGFLDMLVREPSQATAOELLGHPFLKLAGPSCI 709
QY 582 VPLMRQNR 589
DB 710 VPLMRQYR 717
RESULT 14
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ID PAK7 HUMAN
AC Q9P286; Q9BX09; C9ULP6;
DT 16-OCT-2001 (rel. 40, Created)

16-OCT-2001 (rel. 40, last sequence update)
05-JUL-2004 (rel. 44, last annotation update)
Serine/threonine-protein kinase PAK 7 (EC 2.7.1.37) (p21-activated
kinase 7) (PAK-7) (PAK-5).
GN Name=PAK7; Synonyms=KIAA1264, PAK5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22028812; PubMed=12032833; DOI=10.1038/sj/onc/1205478;
RA Pandey A., Dan I., Kristiansen T.Z., Watanabe N.M., Voldby J.,
Kajikawa E., Kiostravi-Far R., Blagoev B., Mann M.,
RT "Cloning and characterization of PAK5, a novel member of mammalian
p21-activated kinase-II subfamily that is predominantly expressed in
brain.";
RT Oncogene 21:3939-3948(2002).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirosewa M., Nomura N.,
Chara O.,
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/141865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
Jones M., Stevisides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A.G., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Elliott A.G., Frankland J.A., Fraser A., French L., Garner P.,
Graffam D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
Hammond E., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Levesaith M.H., Leyzeria M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McCormachie L.J., McIay K., Murray A.A.,
Moline S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prabhalingam S.R., Plumb R.W., Ramsay H.,
Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracy A., Trynans A.C., Vaudin M., Wall M., Wallis J.M.,
Whithead S.L., Whitteker P., Willey D.L., Williams L., Williams S.A.,
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- FUNCTION: The activated kinase acts on a variety of targets (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts tightly with GTP-bound but not GDP-bound
CC CDG42/p21 and Rac1 (by similarity).
CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain.
CC -1- PTM: Autophosphorylated when activated by CDC42/p21 (By
CC similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. STS20
CC subfamily.
CC -1- SIMILARITY: Contains 1 CRIB domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.ebi.ac.uk/announce/>
or send an email to license@ebi.ac.uk).

DR EMBL, AB040812; BAA94194.1; -.
DR EMBL, AB033090; BAA6578.1; ALT_INIT.
DR EMBL, AL353612; CAC34367.1; -.
DR HSSP; Q13153; IFSM.
DR Genew; HGNC:15916; PAK7.
DR H-InVDB; HIX0015637; -.
DR MIM; 608038; -.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/Rho-binding.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR011026; WASF_C.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; P000001; Prot_Kinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00220; STKC; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW transferase.
FT DOMAIN 11 24 CRIB.
FT DOMAIN 25 448 Linker.
FT DOMAIN 449 700 protein kinase.
FT NP_BIND 455 463 ATP (By similarity).
FT BINDING 478 478 ATP (By similarity).
FT ACT_SITE 568 568 Proton acceptor (By similarity).
SQ SEQUENCE 719 AA; 80744 MW; 07A12B1EBC4E2A02 CRC64;

Query Match 56.0%; Score 1731; DB 1; Length 719;
Best Local Similarity 52.4%; Pred. No. 2.7e-56;
Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

1 MFGRKKKEVEISAPENFHRVHTGDFQHEQFTGLPRQMOGLIESARPPKLYDPACIT 60
1 MFGRKKKKKIEISGFENFHRVHTGDFQHEQFTGLPRQMOGLIESARPPKLYDPACIT 60
61 SIQPGAPPTTVYSGKAGDGLTLIDFENNVSITRNSLRDSEPPAPRA-----R 112
61 PQLAPMKTIVYGNPKCKETISNGILDFDNISYTRNSLRKESPPEDQGASSHGPGA 120
113 QENGM-----PEEATTA-----RGG-----PGKA 132
121 EENGEITFSQYSSSEDDTADYTERKREKSLYGDLDPIYRSGSHAAKONGHYMKAGSEA 180
133 -----GSRGEPAGH-----SEAG 145
181 YSEYKPLKSPARKSADYHGHLDLSKPSSEYSDLKWEYGRASSSPIDYSPQFTPSRTA 240
146 GSGGDRRA-----GP-----EKRPYSRESGGPGQESRDKRPISGPDVGT-OPA 191
241 GTSQGSKSLAVSSEWGPISLDYDRRPKSYLANTGSPQTPWR-QRSRSGGGLDEPMMPF 299
192 GLASAKLAAGRPPTY-----PRADTDH-----PERGAGGEHDVAPNGP 232
300 GASAKTTPHQGSYNSYTYPRLSEPTWCIPKVDYDRAQMTLSPLSGS-----DTPKGP 354
233 SAGGLAIPQS-----SSSSSRPPTRAGAPSPGVLGPHASEPQLAPPACTP----- 278
355 A-----KLQSGSKSGYSSSSSHQYPSGCHKA-----TLVNHPSLQSSSQYISTASYLSLSL 406
279 AAPAVGPGPPRPQREFQVSHQFRAALQIVDPGPRSTLYDNFIYIGSGSTGIVCIA 338
407 SSSYTPPPSWGSSSDQGPSRVSHQFRAALQIVVSPGDPREYLANFIKIGSGSTGIVCIA 466

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invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC3, ZC4, KHS2, SUN1, SUN3, GEX2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation, chronic inflammatory disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amyotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiovascular diseases, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants

Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDHOKFTGLPRMOSLIIESARPKPLVDPACIT 60
DB 1 MFGKKRKRVEISAPSNFHRVHTGPDHOKFTGLPRMOSLIIESARPKPLVDPACIT 60
QY 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAEOENGMPEE 120
DB 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAEOENGMPEE 120
QY 121 PATTARGGGKAGSRGRFAGHSEAGGSGDRRRAAGEKPKSRREGSGGPOESSRDKRL 180
DB 121 PATTARGGGKAGSRGRFAGHSEAGGSGDRRRAAGEKPKSRREGSGGPOESSRDKRL 180
QY 181 SGPVGTGPAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAHPNGSAGGLAIP 240
DB 181 SGPVGTGPAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAHPNGSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 300
DB 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 300
QY 301 HEQFRAALQLVVDPGPRSYLDNFIKIGSGTGVCIATVRSNGKLVAVKMDLRKQORR 360
DB 301 HEQFRAALQLVVDPGPRSYLDNFIKIGSGTGVCIATVRSNGKLVAVKMDLRKQORR 360
QY 361 ELLFNEVVIMRDYOHENNVEMTNSYLVGDELWVMEFLGALTDIVTTRANNEQIAAV 420
DB 361 ELLFNEVVIMRDYOHENNVEMTNSYLVGDELWVMEFLGALTDIVTTRANNEQIAAV 420
QY 421 CLAIVTQALSVLHAQGVTHRDIDKSDSILLTHDRVKLSDFGCAQVSKVPRKRSIVGTPY 480
DB 421 CLAIVTQALSVLHAQGVTHRDIDKSDSILLTHDRVKLSDFGCAQVSKVPRKRSIVGTPY 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWYEMWDGSPFYNEBPLKAMKMTIRNLLPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWYEMWDGSPFYNEBPLKAMKMTIRNLLPRLKNLHK 540
QY 541 VSPSLKGLFRLRLVNDPAQATATAEELIKHFLAKAGPPASIVPLMRONTR 591
DB 541 VSPSLKGLFRLRLVNDPAQATATAEELIKHFLAKAGPPASIVPLMRONTR 591

```

RESULT 2
AA59128
ID AA59128 standard; protein; 591 AA.
XX
AC AA59128;
XX
DT 08-MAR-2000 (first entry)

XX Human serine/threonine kinase, PAK4.
DE PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; Rac;
XX Cdc42H; morphogenesis; mitogenesis; JNK; p38 MAP kinase; human;
KW actin polymerization; filopodia; cancer; arthritis.
OS Homo sapiens.
PN WO9963073-A1.
XX 09-DEC-1999.
XX 21-MAY-1999; 99WO-US011341.
PF 21-MAY-1998; 98US-00082737.
PR (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Minden A;
PI WPI, 2000-072881/06.
DR N-PSDB; AA240657.
XX Novel mammalian nucleic acid useful for treating cancer and arthritis.
PT Claim 6; Fig 1A-B; 95pp; English.

The invention relates to an isolated mammalian nucleic acid that encodes PAK4, a novel serine/threonine kinase or its mutant homolog. PAK4 is an effector for the GTPases Rac and Cdc42Hs which are involved in intracellular signal cascades, morphogenesis and mitogenesis, and activate the JNK and p38 MAP kinase pathways. Inhibiting interaction of PAK4 with these enzymes will thus result in inhibition of actin polymerization and formation of filopodia. The PAK4 nucleic acid used for recombinant production of the protein, and as a source of probes for identifying homologous sequences and of (anti)sense oligonucleotides for inhibiting PAK4 expression. The protein, or its fragments, are used to raise specific antibodies and these are useful as ligands for therapeutic inhibition of interaction between PAK4 and its native binding partners. CC Inhibition of PAK4 activity or expression is used for treatment of cancer CC and arthritis. The present sequence represents the human serine/threonine CC kinase, PAK4

Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MFGKKRKRVEISAPSNFHRVHTGPDHOKFTGLPRMOSLIIESARPKPLVDPACIT 60
DB 1 MFGKKRKRVEISAPSNFHRVHTGPDHOKFTGLPRMOSLIIESARPKPLVDPACIT 60
QY 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAEOENGMPEE 120
DB 61 SIOPGAPKTIYVSGSKAGDGLTLLDEFENMSVTRNSLRDSDPPPARAEOENGMPEE 120
QY 121 PATTARGGGKAGSRGRFAGHSEAGGSGDRRRAAGEKPKSRREGSGGPOESSRDKRL 180
DB 121 PATTARGGGKAGSRGRFAGHSEAGGSGDRRRAAGEKPKSRREGSGGPOESSRDKRL 180
QY 181 SGPVGTGPAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAHPNGSAGGLAIP 240
DB 181 SGPVGTGPAGLASGAKLAAGRPFNTYPRADTHPSRGAQGEPHDVAHPNGSAGGLAIP 240
QY 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 300
DB 241 QSSSSSRPPTRARGAPSPGVLGPHASEPOLAPACTPAAPAVPGPPGRSPQREPORVS 300
QY 301 HEQFRAALQLVVDPGPRSYLDNFIKIGSGTGVCIATVRSNGKLVAVKMDLRKQORR 360
DB 301 HEQFRAALQLVVDPGPRSYLDNFIKIGSGTGVCIATVRSNGKLVAVKMDLRKQORR 360

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QY 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLSGALTDIVTTRNMEEOIAAV 420
DB 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLSGALTDIVTTRNMEEOIAAV 420
QY 421 CLAVALQALSVLHAQGIYHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
DB 421 CLAVALQALSVLHAQGIYHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPYPNEPPLKAMKMIKRNLPRLKXNLK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPYPNEPPLKAMKMIKRNLPRLKXNLK 540
QY 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591
DB 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591

RESULT 3
ADC37307
ID ADC37307 standard; protein, 591 AA.
AC ADC37307;
XX
XX
DT 18-DEC-2003 (first entry)
XX
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 140.
XX
XX
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
XX cancer; infectious disease; bone disease; AIDS;
XX neurodegenerative disease; ischemic disorder; Antinflammatory;
XX immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
XX Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
XX
XX Homo sapiens.
XX
XX MO2003048202-A2.
XX
XX 12-JUN-2003.
XX
XX 03-DEC-2002; 2002WO-JP012644.
XX
XX 03-DEC-2001; 2001JP-00368692.
XX
XX 05-DEC-2001; 2001US-0335829P.
XX
XX 03-OCT-2002; 2002JP-00291302.
XX
XX 04-OCT-2002; 2002US-0415769P.
XX
XX
XX (ASAH) ASAMI KASEI KK.
XX
XX PI Matouba A, Muramatsu S;
XX
XX WPI; 2003-505282/47.
XX
XX N-PSDB; ADC37306.
XX
XX
XX New purified protein that activates nuclear factor kappa B (NF-kappaB),
XX useful for treating inflammation, autoimmune diseases, cancer,
XX infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
XX ischemic disorders.
XX
XX Claim 1; SEQ ID NO 140; 938pp; English.
XX
XX
XX The present invention relates to novel proteins and their coding
XX sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
XX kappaB). The proteins and their coding sequences are useful for treating
XX a disease associated with NF-kappaB activation, such as inflammation,
XX autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
XX neurodegenerative diseases, or ischemic disorders.
XX
XX
XX Sequence 591 AA;
XX
XX
XX Query Match 100.0%; Score 3090; DB 7; Length 591;
XX Best local similarity 100.0%; Pred. No. 2,8e-216;
XX Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MFGKKRVEISAPNSFEHRVHTGPDHOKFTGLPRQMSLIBSARRPKPLVDPACIT 60
DB 1 MFGKKRVEISAPNSFEHRVHTGPDHOKFTGLPRQMSLIBSARRPKPLVDPACIT 60
QY 61 SIOPGAPKTIIVGSKGAKGALTLILDEFENNSVTRSNLSLRDPPPPARAGENGMPPE 120
DB 61 SIOPGAPKTIIVGSKGAKGALTLILDEFENNSVTRSNLSLRDPPPPARAGENGMPPE 120
QY 121 PATTARAGPGKAGSGRPFHGBAGGGSGDRRPAAGEKPKSREGSGGPOESSRKRPL 180
DB 121 PATTARAGPGKAGSGRPFHGBAGGGSGDRRPAAGEKPKSREGSGGPOESSRKRPL 180
QY 181 SGPDDVTTPQAGIASAKILAAGRPFNTYPRATDHSRGAQSBPHVANGSAGGLATP 240
DB 181 SGPDDVTTPQAGIASAKILAAGRPFNTYPRATDHSRGAQSBPHVANGSAGGLATP 240
QY 241 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPACTPAAPAVPGPGPRSPQREPORVS 300
DB 241 QSSSSSRPPTARAGAPSPGVLGPHASEPQLAPACTPAAPAVPGPGPRSPQREPORVS 300
QY 301 HEQFRAALQLVDPGDPRSYLDNFIKIGSGTGIACIATVRSKGKLVAVKMDLRKQOR 360
DB 301 HEQFRAALQLVDPGDPRSYLDNFIKIGSGTGIACIATVRSKGKLVAVKMDLRKQOR 360
QY 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLSGALTDIVTTRNMEEOIAAV 420
DB 361 ELLFNEVIMRDYQHENVEMNYSYVGDELWVMEFLSGALTDIVTTRNMEEOIAAV 420
QY 421 CLAVALQALSVLHAQGIYHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
DB 421 CLAVALQALSVLHAQGIYHHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRSKSLVGTPE 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPYPNEPPLKAMKMIKRNLPRLKXNLK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPYPNEPPLKAMKMIKRNLPRLKXNLK 540
QY 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591
DB 541 VSPSLKGFIDRLILVRDPAQRATPAELLKHPFLAKAGPPASIVPLMKONRTR 591

RESULT 4
ADD89973
ID ADD89973 standard; protein, 591 AA.
AC ADD89973;
XX
XX
XX 29-JAN-2004 (first entry)
XX
XX
XX Human cancer-associated protein kinase PAK4.
XX
XX PAK4; protein kinase; enzyme; cancer; cytosolic; immunosuppressive;
XX antidiabetic; antirheumatic; antiarthritic; antipsoriatic;
XX antiangiogenic; antiarteriosclerotic; antiinflammatory; vulnary;
XX gynaecological; neuroprotective; gene therapy; human.
XX
XX Homo sapiens.
XX
XX MO2003083096-A2.
XX
XX 09-OCT-2003.
XX
XX 21-MAR-2003; 2003WO-CA000409.
XX
XX 28-MAR-2002; 2002US-0368853P.
XX
XX (KINE-) KINETEK PHARM INC.
XX
XX Delaney AD;
XX
XX
XX WPI; 2003-833542/77.
XX
XX N-PSDB; ADD89972.

```


XX New nucleic acids encoding cancer associated protein kinases, useful as
PT targets for screening pharmaceutical agents that inhibit the growth of
PT tumor cells, or for diagnosing and treating cancer, inflammation or
PT autoimmune disease.

PS Claim 1, Page 77-78; 91pp; English.

CC The present sequence is the protein sequence of human cancer-associated
CC protein kinase, PAK4. PAK-related kinase PAK4 is an effector molecule for
CC Cdc42Hs. Its gene expression is up-regulated in cancers of the brain,
CC lung, muscle and uterus. PAK4 is one of a set of protein kinases that are
CC shown by the invention to be over-expressed in hyper-proliferative cells.
CC These protein kinases provide targets for drug screening for agents
CC effective in inhibiting the growth or metastasis of tumour cells, and for
CC determining other molecular targets in kinase signal transduction
CC pathways involved in transformation and growth of tumour cells. A claimed
CC method for inhibiting the growth of a cancer cell involves down-
CC regulating the activity of the protein kinase using an antisense sequence
CC or inhibitor of kinase activity, especially where the cancer cell is a
CC breast, liver, colon, muscle, prostate, kidney, lung, placental or
CC uterine cancer cell. Detection of over-expression in cancers provides a
CC useful diagnostic for predicting patient prognosis and probability of
CC drug effectiveness. Agents that specifically bind the protein kinases can
CC be used for treatment and visualisation of tumours in patients. The
CC protein kinase polypeptides and nucleic acids may also be used for
CC treating hyperproliferative diseases, such as autoimmune disease,
CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC atherosclerosis, inflammation, scarring, endometriosis and angiogenesis.

XX Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 7; Length 591;

Best Local Similarity 100.0%; Pred. No. 2.8e-216; Indels 0; Gaps 0;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEOKFTGLPRQWOSLIESARPKPLVDPACT 60
DB 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEOKFTGLPRQWOSLIESARPKPLVDPACT 60
QY 61 SIOPGAPKTIYRSGKAGDGLTLLDEFENMSVTRNSLRDSDPPPARARQENGMPRE 120
DB 61 SIOPGAPKTIYRSGKAGDGLTLLDEFENMSVTRNSLRDSDPPPARARQENGMPRE 120
QY 121 PATTARGGPGKAGRGPRFAGHSEAGSGSDRRRAGPEKRPKSRSGSGGPOESSRDKRPL 180
DB 121 PATTARGGPGKAGRGPRFAGHSEAGSGSDRRRAGPEKRPKSRSGSGGPOESSRDKRPL 180
QY 181 SGPDVGTQPGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
DB 181 SGPDVGTQPGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASBPQLAPPACTPAAPVAPGPPGRRSPQREPORVS 300
DB 241 QSSSSSSRPPTARAGAPSPGVLGPHASBPQLAPPACTPAAPVAPGPPGRRSPQREPORVS 300
QY 301 HEQFAAALQVVDPPGPRSYLNFYKIGSGTGICIAITVRSSGKLVAVKKMDLKKQRR 360
DB 301 HEQFAAALQVVDPPGPRSYLNFYKIGSGTGICIAITVRSSGKLVAVKKMDLKKQRR 360
QY 361 ELTFNEVVIIMDYQHENVEMTNSYLVDGLVWVMEFLGGLTDTIVTHTRNNEQIAAV 420
DB 361 ELTFNEVVIIMDYQHENVEMTNSYLVDGLVWVMEFLGGLTDTIVTHTRNNEQIAAV 420
QY 421 CLAIVQALSVLHAQGVTHRDIKSDSILTLTHDGRVXLSDFGCAQVSKVEPRKSLVGTGY 480
DB 421 CLAIVQALSVLHAQGVTHRDIKSDSILTLTHDGRVXLSDFGCAQVSKVEPRKSLVGTGY 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWYTEMWDGEPVFNENPLKAMKIIDNLPRLKLNHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWYTEMWDGEPVFNENPLKAMKIIDNLPRLKLNHK 540
QY 541 VSPSLKGFIDRLVLVDPQORATAELLKHPLAKAGPPASIVPLMRQNRTR 591

DB 541 VSPSLKGFIDRLVLVDPQORATAELLKHPLAKAGPPASIVPLMRQNRTR 591

RESULT 5
ID ADF45079 standard; protein; 591 AA.

XX ADF45079;

XX 12-FEB-2004 (first entry)

XX Human kinase PAK4.

XX Human; protein kinase; enzyme; inhibitor; PAK4.

XX Homo sapiens.

XX WO2003081210-A2.

XX 02-OCT-2003.

XX 20-MAR-2003; 2003WO-US008725.

XX 21-MAR-2002; 2002US-036682P.

XX (SUNE-) SUNESIS PHARM INC.

XX Prescott JC, Braisted A;

XX WPI; 2003-865136/80.

PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.

PS Disclosure; SEQ ID NO 48; 260pp; English.

CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.

XX Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 7; Length 591;

Best Local Similarity 100.0%; Pred. No. 2.8e-216; Indels 0; Gaps 0;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEOKFTGLPRQWOSLIESARPKPLVDPACT 60
DB 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEOKFTGLPRQWOSLIESARPKPLVDPACT 60
QY 61 SIOPGAPKTIYRSGKAGDGLTLLDEFENMSVTRNSLRDSDPPPARARQENGMPRE 120
DB 61 SIOPGAPKTIYRSGKAGDGLTLLDEFENMSVTRNSLRDSDPPPARARQENGMPRE 120
QY 121 PATTARGGPGKAGRGPRFAGHSEAGSGSDRRRAGPEKRPKSRSGSGGPOESSRDKRPL 180
DB 121 PATTARGGPGKAGRGPRFAGHSEAGSGSDRRRAGPEKRPKSRSGSGGPOESSRDKRPL 180
QY 181 SGPDVGTQPGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
DB 181 SGPDVGTQPGAGLASGAKLAAGRPNNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSSRPPTARAGAPSPGVLGPHASBPQLAPPACTPAAPVAPGPPGRRSPQREPORVS 300


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Db      241 |SSSSSSRPTTARAGAPSGVGLGPHASSEQALPACTPAAPAVPGPGRSRPREQVS 300
Qy      301 |HEGFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQRR 360
Db      301 |HEGFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQRR 360
Qy      361 |ELLFNEVIMRDYQHENVEMTNSYLVDGLVWVMEFLLEGALTDIVTTRNNEEQIAAV 420
Db      361 |ELLFNEVIMRDYQHENVEMTNSYLVDGLVWVMEFLLEGALTDIVTTRNNEEQIAAV 420
Qy      421 |CLAVLOALSVLHAQGYIHRDIKSDSILLTHDGRVKLSDPGFCQVSKVPRKSLVGTPT 480
Db      421 |CLAVLOALSVLHAQGYIHRDIKSDSILLTHDGRVKLSDPGFCQVSKVPRKSLVGTPT 480
Qy      481 |WMAPELISRLPYGPEVDIWSLGIWVLEWVDGEPFYNEPPLKAMKIRDNLPRLKNLHK 540
Db      481 |WMAPELISRLPYGPEVDIWSLGIWVLEWVDGEPFYNEPPLKAMKIRDNLPRLKNLHK 540
Qy      541 |VSPSLKGFIDRLVLRDPAGATATAEILKHPFLAKAGPPASIVPLMKQNRTR 591
Db      541 |VSPSLKGFIDRLVLRDPAGATATAEILKHPFLAKAGPPASIVPLMKQNRTR 591

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RESULT 6
ADH23362
ID ADH23362 standard; protein; 591 AA.

AC ADH23362;

DT 11-MAR-2004 (first entry)

DE Human p21 (CDKN1A)-activated kinase 4 (PAK4) serine/threonine kinase #2.

KM human; p21 (CDKN1A)-activated kinase 4; PAK4; serine/threonine kinase;
KW enzyme; HIV-Tat transcripional activity.

OS Homo sapiens.

PN US2003186254-A1.

PD 02-OCT-2003.

PF 29-APR-2002; 2002US-00134102.

PR 30-DEC-1999; 99US-0173939P.

PR 28-DEC-2000; 2000US-00750457.

PA (CELL-) CELL SIGNALING TECHNOLOGY INC.

PI Melnick MB, Moritz A, Comb MJ;

DR WPI; 2004-130707/13.

DR N-PSDB; ADH23361.

PT New isolated DNA sequence encoding PAK4 serine/threonine kinase for
modulating the transcriptional activity of human immunodeficiency virus-
Tat protein.

PS Example 1; SEQ ID NO 4; 47pp; English.

CC The invention relates to an isolated DNA sequence encoding p21 (CDKN1A)-
activated kinase 4 (PAK4) serine/threonine kinase. The invention is
useful for modulating the transcriptional activity of HIV-Tat protein.
CC The invention provides isolated DNA and vectors encoding PAK4 and Cdc42-
GEP which synergize to stimulate Tat transcriptional activity. The
CC present sequence represents the amino acid sequence of human PAK4.

SQ Sequence 591 AA;

Query Match 100.0%; Score 3090; DB 8; Length 591;
Best Local Similarity 100.0%; Pred. No. 2,8e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 |MEGKKRVEISAPSNFEHRVHTGPDHOKETGLPRQWOSLIIESARRPKPLVDPACT 60
Db      1 |MFGKKRVEISAPSNFEHRVHTGPDHOKETGLPRQWOSLIIESARRPKPLVDPACT 60
Qy      61 |SIOPGAPKTIIVGSKAKDGAATLLIDPEFNNSVTSNSLRDSDPPPARAQENQMPPE 120
Db      61 |SIOPGAPKTIIVGSKAKDGAATLLIDPEFNNSVTSNSLRDSDPPPARAQENQMPPE 120
Qy      121 |PATTAGGPKKAGSRGFAGHSBAAGSGSDRRRPADEKPKSSREGSGGPOESSRDKPL 180
Db      121 |PATTAGGPKKAGSRGFAGHSBAAGSGSDRRRPADEKPKSSREGSGGPOESSRDKPL 180
Qy      181 |SGPDVCTPPAGLAASAKLAAGRPFNTYPRATDHSRGAQEPHDVANGSPAGGLATP 240
Db      181 |SGPDVCTPPAGLAASAKLAAGRPFNTYPRATDHSRGAQEPHDVANGSPAGGLATP 240
Qy      241 |QSSSSSRPPTARAGAPSGVGLGPHASSEQALPACTPAAPAVPGPGRSRPREQVS 300
Db      241 |QSSSSSRPPTARAGAPSGVGLGPHASSEQALPACTPAAPAVPGPGRSRPREQVS 300
Qy      301 |HEGFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQRR 360
Db      301 |HEGFRAALQLVVDPGDPRSYLDNFIKIGEGSTGIVCIATVRSSGKLVAVKXMDLRKQRR 360
Qy      361 |ELLFNEVIMRDYQHENVEMTNSYLVDGLVWVMEFLLEGALTDIVTTRNNEEQIAAV 420
Db      361 |ELLFNEVIMRDYQHENVEMTNSYLVDGLVWVMEFLLEGALTDIVTTRNNEEQIAAV 420
Qy      421 |CLAVLOALSVLHAQGYIHRDIKSDSILLTHDGRVKLSDPGFCQVSKVPRKSLVGTPT 480
Db      421 |CLAVLOALSVLHAQGYIHRDIKSDSILLTHDGRVKLSDPGFCQVSKVPRKSLVGTPT 480
Qy      481 |WMAPELISRLPYGPEVDIWSLGIWVLEWVDGEPFYNEPPLKAMKIRDNLPRLKNLHK 540
Db      481 |WMAPELISRLPYGPEVDIWSLGIWVLEWVDGEPFYNEPPLKAMKIRDNLPRLKNLHK 540
Qy      541 |VSPSLKGFIDRLVLRDPAGATATAEILKHPFLAKAGPPASIVPLMKQNRTR 591
Db      541 |VSPSLKGFIDRLVLRDPAGATATAEILKHPFLAKAGPPASIVPLMKQNRTR 591

```

RESULT 7

ID ABM82101 standard; protein; 591 AA.

AC ABM82101;

DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) polypeptide PRO61458, SEQ:5422.

KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;

KM tumour; diagnosis; cell proliferative disorder; breast cancer;

KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KM central nervous system cancer; bladder cancer; pancreatic cancer;

KM cervical cancer; melanoma; leukaemia; hybridisation probe;

KM chromosome identification; chromosome mapping; gene mapping;

OS Homo sapiens.

PN WO2004030615-A2.

PD 15-APR-2004.

PF 29-SEP-2003; 2003WO-US028547.

PR 02-OCT-2002; 2002US-0414971P.

PA (GETH) GENENTECH INC.

PI Wu TD, Zhang Z, Zhou Y;

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XX MPI; 2004-347921/32.
DR N-PSDB; ACN40564.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 5422; 7273bp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acids and
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment or
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
XX antibodies, antagonists, binding molecules and compositions are useful
XX for diagnosing or treating a cell proliferative disorder associated with
XX increased TAT expression, particularly cancers such as breast cancer,
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX cancer, pancreatic cancer, cervical cancer, cancers of the central
XX nervous system, melanoma and leukemia. TAT nucleic acids may further be
XX used as hybridisation probes, in chromosome and gene mapping, in
XX chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention
XX
XX Sequence 591 AA;
SQ
Query Match 100.0%; Score 3090; DB 8; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVPACT 60
DB 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVPACT 60
QY 61 SIQCAPKTIYVSGSKAGKDALTLTLLDEFENMSVTRNSLRDSDPPPARAQENGMEE 120
DB 61 SIQCAPKTIYVSGSKAGKDALTLTLLDEFENMSVTRNSLRDSDPPPARAQENGMEE 120
QY 121 PATTARGGPRKAGSGRFRAGHSEAGGSDRRARAPKPKSSRRGSGGPGSSSDKRL 180
DB 121 PATTARGGPRKAGSGRFRAGHSEAGGSDRRARAPKPKSSRRGSGGPGSSSDKRL 180
QY 181 SGPVGTGPQAGLAGAKLAAGRPNFTYPRADTDHPSRGAQGEPRDVA PNGSAGALAI 240
DB 181 SGPVGTGPQAGLAGAKLAAGRPNFTYPRADTDHPSRGAQGEPRDVA PNGSAGALAI 240
QY 241 QSSSSSSRPPTRARAPSPGVIGPHASEPQOLAPACTPAAPAVPCPGPRSPQRPQVS 300
DB 241 QSSSSSSRPPTRARAPSPGVIGPHASEPQOLAPACTPAAPAVPCPGPRSPQRPQVS 300
QY 301 HEOPFAALQLVDPDPSYLDNFKITIGEGSTGICATVSSSGKLVA VKMDLKKQRR 360
DB 301 HEOPFAALQLVDPDPSYLDNFKITIGEGSTGICATVSSSGKLVA VKMDLKKQRR 360
QY 361 ELLFNEVIMEDYGHENVENWNTSYLVGDELWVMELEGALITDIYVTHTRNNEQIAV 420
DB 361 ELLFNEVIMEDYGHENVENWNTSYLVGDELWVMELEGALITDIYVTHTRNNEQIAV 420
QY 421 CLAVIQALSVLHAQGVIRHDIKSDSILLTHDGRVTLSDFGCAQVSKVPRRKSIVGTPY 480
DB 421 CLAVIQALSVLHAQGVIRHDIKSDSILLTHDGRVTLSDFGCAQVSKVPRRKSIVGTPY 480
QY 481 WMAPELISRLPYGPEVDIWSIGIMTWIEMVVDGPPFENPPLKAMKMTDNLPPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSIGIMTWIEMVVDGPPFENPPLKAMKMTDNLPPRLKNLHK 540
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QY 541 VSPSLKGFUDRLVDPAPORATAAELLKHPPLAKGPPASTVPLMRQNR 591
DB 541 VSPSLKGFUDRLVDPAPORATAAELLKHPPLAKGPPASTVPLMRQNR 591
RESULT 8
ABG19308
ID ABG19308 standard; protein, 620 AA.
XX
XX ABG19308;
AC
XX
XX 18-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #19299.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSSE-) HYSSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX
XX MPI; 2001-639362/73.
XX
XX N-PSDB; AAS83495.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 49667; 1033p; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pcl_sequences
XX
XX Sequence 620 AA;
SQ
Query Match 100.0%; Score 3090; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 2.9e-216;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVPACT 60
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Db      30 MEGKRRKRVETISAPSNFEHRVHTGPDHQKFTGLPRQMSLIEESARRPKPLVDACIT 89
Qy      61 STPGAPKTIYVSGSKAKGALTLLIDDEFENNSVTRNSLRDSDPPPPARAOENGMPEE 120
Db      90 STPGAPKTIYVSGSKAKGALTLLIDDEFENNSVTRNSLRDSDPPPPARAOENGMPEE 149
Qy      121 PATTARAGGPKAGSRGRFAGHSEAGGSDRRRAGGPKPKSREGSGGPOESSRDKRPL 180
Db      150 PATTARAGGPKAGSRGRFAGHSEAGGSDRRRAGGPKPKSREGSGGPOESSRDKRPL 209
Qy      181 SGPDVGTPOGAGIAGAKLAAGRPENTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 240
Db      210 SGPDVGTPOGAGIAGAKLAAGRPENTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 269
Qy      241 QSSSSSSRPPTARAGAPSPGVGPHASEPQLAPPAAPVAPGPPGRSPRREPQRVS 300
Db      270 QSSSSSSRPPTARAGAPSPGVGPHASEPQLAPPAAPVAPGPPGRSPRREPQRVS 329
Qy      301 HEOPRAALQLVDPGDPGRSYLNFRTKIGSGSTGIVCIATVRSRSGKVAAYKMDLRQQR 360
Db      330 HEOPRAALQLVDPGDPGRSYLNFRTKIGSGSTGIVCIATVRSRSGKVAAYKMDLRQQR 389
Qy      361 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLGAGALTDIVTTRNMEQIAAV 420
Db      390 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLGAGALTDIVTTRNMEQIAAV 449
Qy      421 CLAVALQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPE 480
Db      450 CLAVALQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPE 509
Qy      481 WMAPELISRLPYGPEVDISLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 540
Db      510 WMAPELISRLPYGPEVDISLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 569
Qy      541 VSPSLKGFDRLLVNDPAPQATATAEILKHPFLAKAGPPASIVPLMKQNTR 591
Db      570 VSPSLKGFDRLLVNDPAPQATATAEILKHPFLAKAGPPASIVPLMKQNTR 620

RESULT 9
ADH23359
ID      ADH23359 standard; protein; 588 AA.
XX
AC      ADH23359;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Human p21 (CDKN1A)-activated kinase 4 (PAK4) serine/threonine kinase #1.
XX
KW      human; p21 (CDKN1A)-activated kinase 4; PAK4; serine/threonine kinase;
KM      enzyme; HIV-Tat transcriptional activity.
XX
OS      Homo sapiens.
XX
PN      US2003186254-A1.
XX
PD      02-OCT-2003.
XX
PF      29-APR-2002; 2002US-00134102.
XX
PR      30-DEC-1999; 99US-0173939P.
XX      PR      28-DEC-2000; 2000US-00750457.
XX
PA      (CELL-) CELL SIGNALING TECHNOLOGY INC.
XX
PI      Melnick MB, Moritz A, Comb MJ;
XX
DR      WPI; 2004-130707/13.
XX      DR      N-PSDB; ADH23361.
XX
PT      New isolated DNA sequence encoding PAK4 serine/threonine kinase for
modulating the transcriptional activity of human immunodeficiency virus-

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PT      Tat protein.
XX
XX      Claim 1; SEQ ID NO 1; 47bp; English.
XX
CC      The invention relates to an isolated DNA sequence encoding p21 (CDKN1A)-
CC      activated kinase 4 (PAK4) serine/threonine kinase. The invention is
CC      useful for modulating the transcriptional activity of HIV-Tat protein.
CC      The invention provides isolated DNA and vectors encoding PAK4 and Cdc42-
CC      GEF which synergize to stimulate Tat transcriptional activity. The
CC      present sequence represents the amino acid sequence of human PAK4.
XX
SQ      Sequence 588 AA;
XX
Query Match      99.5%; Score 3075; DB 8; Length 588;
Best Local Similarity 100.0%; Pred No. 3.4e-215;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEGKRRKRVETISAPSNFEHRVHTGPDHQKFTGLPRQMSLIEESARRPKPLVDACIT 60
Db      1 MEGKRRKRVETISAPSNFEHRVHTGPDHQKFTGLPRQMSLIEESARRPKPLVDACIT 60
Qy      61 STPGAPKTIYVSGSKAKGALTLLIDDEFENNSVTRNSLRDSDPPPPARAOENGMPEE 120
Db      61 STPGAPKTIYVSGSKAKGALTLLIDDEFENNSVTRNSLRDSDPPPPARAOENGMPEE 120
Qy      121 PATTARAGGPKAGSRGRFAGHSEAGGSDRRRAGGPKPKSREGSGGPOESSRDKRPL 180
Db      121 PATTARAGGPKAGSRGRFAGHSEAGGSDRRRAGGPKPKSREGSGGPOESSRDKRPL 180
Qy      181 SGPDVGTPOGAGIAGAKLAAGRPENTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 240
Db      181 SGPDVGTPOGAGIAGAKLAAGRPENTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIP 240
Qy      241 QSSSSSSRPPTARAGAPSPGVGPHASEPQLAPPAAPVAPGPPGRSPRREPQRVS 300
Db      241 QSSSSSSRPPTARAGAPSPGVGPHASEPQLAPPAAPVAPGPPGRSPRREPQRVS 300
Qy      301 HEOPRAALQLVDPGDPGRSYLNFRTKIGSGSTGIVCIATVRSRSGKVAAYKMDLRQQR 360
Db      301 HEOPRAALQLVDPGDPGRSYLNFRTKIGSGSTGIVCIATVRSRSGKVAAYKMDLRQQR 360
Qy      361 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLGAGALTDIVTTRNMEQIAAV 420
Db      361 ELLFNEVIMRDYOHENNVEMVNSYLVDLWVMEFLGAGALTDIVTTRNMEQIAAV 420
Qy      421 CLAVALQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPE 480
Db      421 CLAVALQALSVLHAQGVYHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPE 480
Qy      481 WMAPELISRLPYGPEVDISLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 540
Db      481 WMAPELISRLPYGPEVDISLGIWVEMWDGEPYNEPPLKMKMIRDLNLPRLKNLHK 540
Qy      541 VSPSLKGFDRLLVNDPAPQATATAEILKHPFLAKAGPPASIVPLMKQNTR 588
Db      541 VSPSLKGFDRLLVNDPAPQATATAEILKHPFLAKAGPPASIVPLMKQNTR 588

RESULT 10
ADJ96654
ID      ADJ96654 standard; protein; 593 AA.
XX
AC      ADJ96654;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Human sterile protein kinase STE20 Paks_m protein Seqid 111.
XX
KW      kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KM      PTK; STK; gene therapy; cancer; immune-related disease; metabolic;
KM      cardiovascular disease; brain; neuronal associated disease; inflammatory
disorder; cytostatic; neuroprotective; immunomodulator;
KM      antiinflammatory; enzyme; sterile protein kinase STE20; Paks_m.

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XX Homo sapiens.
 OS 59.
 PN WO2004006838-A2.
 PD 22-JAN-2004.
 PF 15-JUL-2003; 2003WO-US021730.
 PR 15-JUL-2002; 2002US-0395632P.
 XX (SUGB-) SUGEN INC.
 PI Whyte D, Manning G, Caenepeel S;
 DR WPI: 2004-122753/12.
 DR N-PSDB; ADJ96588.
 XX New nucleic acid molecule encoding a kinase polypeptide, useful for
 PT preparing a composition for treating diseases or disorders, e.g., cancer,
 PT or neurological, immunological or inflammatory disorders.
 PS Claim 1; SEQ ID NO 111; 366pp; English.
 XX This invention relates to a novel isolated, enriched or purified nucleic
 CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
 CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
 CC as well as protein kinase-like enzymes. The present invention describes
 CC screening methods to identify agonists, antagonists and antibodies that
 CC can be used to modulate the activity or function of the mammalian kinase
 CC enzymes. As such, these compositions can be used for gene therapy
 CC purposes to treat diseases or disorders including cancer, immune-related
 CC diseases, cardiovascular disease, brain or neuronal associated disease,
 CC metabolic and inflammatory disorders. Accordingly, they exhibit
 CC cytostatic, neuroprotective, immunomodulator and anti-inflammatory
 CC activities. This polypeptide sequence is a human kinase protein sequence
 CC of the invention.
 XX Sequence 593 AA;
 SQ
 Query Match 92.6%; Score 2860; DB 8; Length 593;
 Best Local Similarity 92.6%; Pred. No. 1.5e-199;
 Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;
 QY 1 MFGKKRRVEISAPSNFEHRVHTGPDHOKFTGLPRQMSLIESARRPKVLDPACT 60
 DB 1 MFGKKRRVEISAPSNFEHRVHTGPDHOKFTGLPRQMSLIESARRPKVLDPACT 60
 QY 61 SIQPGAPKTIIVGSKAGKADALTLILDEFENMSVTRNSLRRDSPPPRARQENGMPEE 120
 DB 61 SIQPGAPKTIIVGSKAGKADALTLILDEFENMSVTRNSLRRDSPPPRARQENGMPEE 120
 QY 121 PATTARGGCGKSGKRFAGSHBAGGSGDRRRAPBEKPKSSRGGSGPQSSRDKRL 180
 DB 121 RAAPARMAPDKAGSRRARATGSHSEAGSGDRRRVGEKEPKSSRDGPGQASDKRPL 180
 QY 181 SGPDVGTGPAGIAGAKXLAAGRPFNTYPRADTDHPSRGAQSEPHDVANNGSAGSLAP 240
 DB 181 SGPDVGTGPAGIAGAKXLAAGRPFNTYPRADTDHPSRGAQSEPHDVANNGSAGSLAP 240
 QY 241 QSSSSSSRPPTARAGAPSPGVLPAPASEPOLAPPA---CTPAAPAVPGPPGRRSPQREPO 297
 DB 241 QSSSSSSRPPTARAGAPSPGVLPAPASEPOLAPPA---CTPAAPAVPGPPGRRSPQREPO 297
 QY 298 RVSHQGFRAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 357
 DB 298 RVSHQGFRAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 357
 QY 359 RYSHQGFRAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 359
 DB 359 RYSHQGFRAALQLVVDPPGPRSYLDNFIKIGSGSTGIVCIATVRSSGKLVAVKMDLRKQ 359
 QY 417 ORRELLFNEVIMRDYOHENNVEMTNSYLVPDELVWVEFLGALTLIDVTHTRNNEEI 417
 DB 417 ORRELLFNEVIMRDYOHENNVEMTNSYLVPDELVWVEFLGALTLIDVTHTRNNEEI 417

QY 418 AAVCLAVIALSALVHAQGVIRHDIKSDSILTLTHDGRVXLSDFGCAQVSKVPRRRKSLVG 477
 DB 420 AAVCLAVIALVHAQGVIRHDIKSDSILTLTHDGRVXLSDFGCAQVSKVPRRRKSLVG 479
 QY 478 TPYMAPELISRLPYGPEVDIWSLGIWYIEMVDGPPYFNNEPPLKAMKIRNLPPRLKN 537
 DB 480 TPYMAPELISRLPYGPEVDIWSLGIWYIEMVDGPPYFNNEPPLKAMKIRNLPPRLKN 539
 QY 538 LHKVPSLKGFLDRLVDPAPQATRAELKHPFLAKGPPASIVPLMRQNRTR 591
 DB 540 LHKVPSLKGFLDRLVDPAPQATRAELKHPFLAKGPPASIVPLMRQNRTR 593
 RESULT 11
 ID ABM84642 standard; protein; 522 AA.
 AC ABM84642;
 XX 18-NOV-2004 (first entry)
 DR Human diagnostic and therapeutic protein SEQ ID NO:4891.
 DE gene therapy; human diagnostic and therapeutic polynucleotide; ditbp.
 XX Homo sapiens.
 XX WO2004023973-A2.
 PD 25-MAR-2004.
 PF 12-SEP-2003; 2003WO-US028227.
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gershtin EH;
 PI Peralta CH, Anderson SB, Ricoux P, Shen EJ, Wu MC, Stuve LJ;
 PI Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Pacury S, Shi X, Suarez CJ;
 XX WPI: 2004-329368/30.
 DR N-PSDB; ACN43294.
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 PS Claim 27; Page; 190pp; English.
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (ditbp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The ditbp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line
 CC gene therapy. The present sequence represents a ditbp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 522 AA;
 SQ Query Match 86.6%; Score 2674.5; DB 8; Length 522;
 Best Local Similarity 88.2%; Pred. No. 4.2e-186;
 Matches 521; Conservative 0; Mismatches 1; Indels 69; Gaps 1;

QY 1 MFGKRRKRVEISAPSNFHRVHTGPDQHKFTGLPRQMSLIESARPKPLVDACIT 60
 DB 1 MFGKRRKRVEISAPSNFHRVHTGPDQHKFTGLPRQMSLIESARPKPLVDACIT 60

QY 61 SIOPGAPKTIYVSGSKAGKAGALTLILDEFENNSVTRNSLRDPPPARAQENGMPEE 120
 DB 61 SIOPGAPKTIYVSGSKAGKAGALTLILDEFENNSVTRNSLRDPPPARAQENGMPEE 120

QY 121 PATTARGGGKAGSKRGKRFAGHSEAGGSGDRRRAGEKPKSRGSGGQESSRDKRL 180
 DB 121 PATT----- 124

QY 181 SGPDVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPPHDVAPNGSPAGLAI 240
 DB 125 -----AKGAKLAAGRPNTYPRADTDHPSRGAQGEPPHDVAPNGSPAGLAI 171

QY 241 QSSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORVS 300
 DB 172 QSSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORVS 231

QY 301 HEQFRAALQLVDPDPDSYLDNFIKIGSGTICVCIATVRSSGKLVAVKMDLRKQRR 360
 DB 233 HEQFRAALQLVDPDPDSYLDNFIKIGSGTICVCIATVRSSGKLVAVKMDLRKQRR 291

QY 361 ELLFNEVIMRDYQHENVNEMNSYLVDGLVWVEFLGGLTDTVTHRNNEEOIAV 420
 DB 292 ELLFNEVIMRDYQHENVNEMNSYLVDGLVWVEFLGGLTDTVTHRNNEEOIAV 351

QY 421 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKKSIVGT 480
 DB 352 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKKSIVGT 411

QY 481 WMAPELISRLPYGPEVDIVSLGIMVIEWDGEPYNEPPLKAMKIRDNLPRLKNLHK 540
 DB 412 WMAPELISRLPYGPEVDIVSLGIMVIEWDGEPYNEPPLKAMKIRDNLPRLKNLHK 471

QY 541 VSPSLKGFRLDLLVDPDAQRATTAELKHPFLAKGPPASIVPLMKQNRTR 591
 DB 472 VSPSLKGFRLDLLVDPDAQRATTAELKHPFLAKGPPASIVPLMKQNRTR 522

RESULT 12
 ABM84644
 ID ABM84644 standard; protein; 522 AA.
 AC ABM84644;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO: 4893.
 XX
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 XX
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
 PI Harthorne TA, Suchorski MT, Altus CM, Pits SJ, Rider LV,
 PI Mooney EM, Deleage AM, Pansar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RB, Spiro PA, Stewart EA, Wingrove J, Valt UA, Kitron ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patuay S, Shi X, Share CJ;
 XX
 DR MPI, 2004-329368/30.
 DR N-PSDB; ACN43296.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm
 CC
 SQ Sequence 522 AA;
 Query Match 86.6%; Score 2674.5; DB 8; Length 522;
 Best Local Similarity 88.2%; Pred. No. 4.2e-186;
 Matches 521; Conservative 0; Mismatches 1; Indels 69; Gaps 1;

QY 1 MFGKRRKRVEISAPSNFHRVHTGPDQHKFTGLPRQMSLIESARPKPLVDACIT 60
 DB 1 MFGKRRKRVEISAPSNFHRVHTGPDQHKFTGLPRQMSLIESARPKPLVDACIT 60

QY 61 SIOPGAPKTIYVSGSKAGKAGALTLILDEFENNSVTRNSLRDPPPARAQENGMPEE 120
 DB 61 SIOPGAPKTIYVSGSKAGKAGALTLILDEFENNSVTRNSLRDPPPARAQENGMPEE 120

QY 121 PATTARGGGKAGSKRGKRFAGHSEAGGSGDRRRAGEKPKSRGSGGQESSRDKRL 180
 DB 121 PATT----- 124

QY 181 SGPDVGTGPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPPHDVAPNGSPAGLAI 240
 DB 125 -----AKGAKLAAGRPNTYPRADTDHPSRGAQGEPPHDVAPNGSPAGLAI 171

QY 241 QSSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORVS 300
 DB 172 QSSSSSSRPPTARAGAPSPGVLPASBPOLAPACTPAAPAVPGPGRSPQREPORVS 231

QY 301 HEQFRAALQLVDPDPDSYLDNFIKIGSGTICVCIATVRSSGKLVAVKMDLRKQRR 360
 DB 233 HEQFRAALQLVDPDPDSYLDNFIKIGSGTICVCIATVRSSGKLVAVKMDLRKQRR 291

QY 361 ELLFNEVIMRDYQHENVNEMNSYLVDGLVWVEFLGGLTDTVTHRNNEEOIAV 420
 DB 292 ELLFNEVIMRDYQHENVNEMNSYLVDGLVWVEFLGGLTDTVTHRNNEEOIAV 351

QY 421 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKKSIVGT 480
 DB 352 CLAVLQALSVLAAGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKKSIVGT 411

QY 481 WMAPELISRLPYGPEVDIWSLGIWVLEMDGEPFYFNEPPLKAMKIMRDNLPRLKNLHK 540
 DB 412 WMAPELISRLPYGPEVDIWSLGIWVLEMDGEPFYFNEPPLKAMKIMRDNLPRLKNLHK 471
 QY 541 VSPSLKGFILRLVDPQATATAEELKHPFLAKAGPPASIVPLMKQRNTR 591
 DB 472 VSPSLKGFILRLVDPQATATAEELKHPFLAKAGPPASIVPLMKQRNTR 522

RESULT 13
 AEM84645
 ID AEM84645 standard; protein; 522 AA.
 XX AEM84645;
 AC AEM84645;
 XX 18-NOV-2004 (first entry)
 DT Human diagnostic and therapeutic pprotein SEQ ID NO:4894.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4894.
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
 KM Homo sapiens.
 OS
 XX WO2004023973-A2.
 PN 25-MAR-2004.
 XX 12-SEP-2003; 2003WO-US028227.
 PF 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Sterens KA, Blanchard JT, Panesar SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Valt UA, Klinton ES;
 PI Xu Y, Kwong M, Policky JT, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patuty S, Shi X, Suarez CJ;
 XX
 DR MPI: 2004-329368/30.
 DR N-PSDB; ACN43297.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorders,
 CC infections caused by virus, bacteria, fungi or parasite. The dittp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dittp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 CC
 XX Sequence 522 AA;
 SQ

Query Match 86.6%; Score 2674.5; DB 8; Length 522;
 Best Local Similarity 88.2%; Pred. No. 4.2e-186;
 Matches 521; Conservative 0; Mismatches 1; Indels 69; Gaps 1;

QY 1 MFGKKRKEVEISAPNPFHRVHTGPDQHEOKFTGLPRWQOSIIESSARRKPLVDPACIT 60
 DB 1 MFGKKRKEVEISAPNPFHRVHTGPDQHEOKFTGLPRWQOSIIESSARRKPLVDPACIT 60
 QY 61 SIQGPAPKTIYRGSAGADGALLTLIDDEFENNSVTRNSLRDSSPPAPARQENGMEE 120
 DB 61 SIQGPAPKTIYRGSAGADGALLTLIDDEFENNSVTRNSLRDSSPPAPARQENGMEE 120
 QY 121 PATTARGGPKAGSKRGPRAGHSEAGSGSDRRRAGPEKRRPKSSRBSGGQPOESSRDKPL 180
 DB 121 PATTARGGPKAGSKRGPRAGHSEAGSGSDRRRAGPEKRRPKSSRBSGGQPOESSRDKPL 180
 QY 181 SGPDVGTQPPAGLASGATLAAGRPPNTYPRADTDHPSGAGCEPHDVAHPNGSAGGLAIP 240
 DB 181 SGPDVGTQPPAGLASGATLAAGRPPNTYPRADTDHPSGAGCEPHDVAHPNGSAGGLAIP 240
 QY 125 -----AAGATLAAGRPPNTYPRADTDHPSGAGCEPHDVAHPNGSAGGLAIP 171
 DB 125 -----AAGATLAAGRPPNTYPRADTDHPSGAGCEPHDVAHPNGSAGGLAIP 171
 QY 241 OSSSSSRPPTRRARGAPSGVLTGPHASRROLAPACTPAAPVAPGPPRSPORRORS 300
 DB 172 OSSSSSRPPTRRARGAPSGVLTGPHASRROLAPACTPAAPVAPGPPRSPORRORS 231
 QY 301 HEQFRAALQVLVDPDPRSYLDNFIKIGEGSTGIVCIATVSSGCLVAVKMDLKKQQR 360
 DB 232 HEQFRAALQVLVDPDPRSYLDNFIKIGEGSTGIVCIATVSSGCLVAVKMDLKKQQR 291
 QY 361 ELLFNEVYIMRDYQHENNVEMNSYLVDDELWVMEFLEGALTDIVHTRNNEQIAAV 420
 DB 232 ELLFNEVYIMRDYQHENNVEMNSYLVDDELWVMEFLEGALTDIVHTRNNEQIAAV 351
 QY 421 CLAVLQALSYVAQGVHHRDIKSDSILTLHDGRVLTSPFGCAQYSKEVPRKSLVGTPT 480
 DB 352 CLAVLQALSYVAQGVHHRDIKSDSILTLHDGRVLTSPFGCAQYSKEVPRKSLVGTPT 411
 QY 481 WMAPELISRLPYGPEVDIWSLGIWVLEMDGEPFYFNEPPLKAMKIMRDNLPRLKNLHK 540
 DB 412 WMAPELISRLPYGPEVDIWSLGIWVLEMDGEPFYFNEPPLKAMKIMRDNLPRLKNLHK 471
 QY 541 VSPSLKGFILRLVDPQATATAEELKHPFLAKAGPPASIVPLMKQRNTR 591
 DB 472 VSPSLKGFILRLVDPQATATAEELKHPFLAKAGPPASIVPLMKQRNTR 522

RESULT 14
 AEM84648
 ID AEM84648 standard; protein; 517 AA.
 XX AEM84648;
 AC AEM84648;
 XX 18-NOV-2004 (first entry)
 DT Human diagnostic and therapeutic pprotein SEQ ID NO:4897.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4897.
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
 KM Homo sapiens.
 OS
 XX WO2004023973-A2.
 PN 25-MAR-2004.
 PF 12-SEP-2003; 2003WO-US028227.
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geregin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Viltc UA, Kitron ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CU;
 DR MPI; 2004-329368/30.
 DR N-PSDB; ACN43300.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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 XX
 XX Claim 27; Page: 190pp; English.
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 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
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 CC disorders, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 CC
 XX
 XX Sequence 517 AA;

Query Match 86.1%; Score 2662; DB 8; Length 517;
 Best Local Similarity 87.3%; Pred. No. 3, 4e-185;
 Matches 516; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

QY 1 MFGKRRKRVISAPSNFEHRVHTGFDHOKFTGLPRQMSLIESARRPKPLVDACIT 60
 DB 1 MFGKRRKRVISAPSNFEHRVHTGFDHOKFTGLPRQMSLIESARRPKPLVDACIT 60
 QY 61 STGPAPKTIYVSGSKAKGALTLLDFEENMSVTSNSLRSDPPPPARAQENMPRE 120
 DB 61 STGPAPKTIYVSGSKAKGALTLLDFEENMSVTSNSLRSDPPPPARAQENMPRE 120
 QY 121 PATTARAGPGKAGSRGFRGSHSAGGSGDRRAAGPEKPKSRRBSGGPQSSSRDKEPL 180
 DB 121 PATTARAGPGKAGSRGFRGSHSAGGSGDRRAAGPEKPKSRRBSGGPQSSSRDKEPL 180
 QY 181 SGPDVGTPOPAAGIAGAKLAAGRPFTYPRADTHPSRGAOGEPHDVAPNGSPAGLAIP 240
 DB 181 SGPDVGTPOPAAGIAGAKLAAGRPFTYPRADTHPSRGAOGEPHDVAPNGSPAGLAIP 240
 QY 241 QSSSSSSRPPTARAKAPSGVAGPHASEPOLAPACTPAAPAVPGPPGPPRRRQRYX 300
 DB 241 QSSSSSSRPPTARAKAPSGVAGPHASEPOLAPACTPAAPAVPGPPGPPRRRQRYX 300
 QY 301 HGFOPRALQLVDPGPRSYLDNFIFIKIGSGSTGIVICATVRSRSGKVAVYKMDLRQQR 360
 DB 301 HGFOPRALQLVDPGPRSYLDNFIFIKIGSGSTGIVICATVRSRSGKVAVYKMDLRQQR 360
 QY 361 ELLFNEVIMRDYOHENVMNTSYLVGDELWVMELEGALTDIVTHTRMNEOIAAV 420
 DB 361 ELLFNEVIMRDYOHENVMNTSYLVGDELWVMELEGALTDIVTHTRMNEOIAAV 420
 QY 421 CLAVALQALSVLAHQGVYIHRDIKSDSLILTHDRVVKLSDPFCQVSKVPRKSLVGT 480
 DB 421 CLAVALQALSVLAHQGVYIHRDIKSDSLILTHDRVVKLSDPFCQVSKVPRKSLVGT 480
 QY 481 WMAPELISRLPYGPEVDIWSLGMVTEWVDEGPYENEPPLKMKKIRIINPLRLNKLK 540
 DB 481 WMAPELISRLPYGPEVDIWSLGMVTEWVDEGPYENEPPLKMKKIRIINPLRLNKLK 540

DB 407 WMAPELISRLPYGPEVDIWSLGMVTEWVDEGPYENEPPLKMKKIRIINPLRLNKLK 466
 QY 541 VSPSLKGFILRLNDDPAORATRAELIKHPLAKGPPASTIPLMRQNT 591
 DB 467 VSPSLKGFILRLNDDPAORATRAELIKHPLAKGPPASTIPLMRQNT 517

RESULT 15

ID ABM84647 standard; protein; 517 AA.

AC ABM84647;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4896.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

OS Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marinovic MM, Shen P;

XX Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Sider LV;

XX Mooney EM, Delegeane IS, Banville SC, Reddy TP;

XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geregin EH;

XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;

XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Viltc UA, Kitron ES;

XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX Patury S, Shi X, Suarez CU;

PS Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorders, endocrine
 CC disorders, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 CC
 XX
 XX Sequence 517 AA;

Query Match 86.1%; Score 2662; DB 8; Length 517;
 Best Local Similarity 87.3%; Pred. No. 3, 4e-185;
 Matches 516; Conservative 0; Mismatches 1; Indels 74; Gaps 1;

QY 1 MFGRRKRVHISAPSNFHRVHTGFDQHEQKFTGLPRWQSLIESARPKPLVDPACT 60
Db 1 MFGRRKRVHISAPSNFHRVHTGFDQHEQKFTGLPRWQSLIESARPKPLVDPACT 60
QY 61 SIOPGAPKTIIVRSKSKAKOGALTLILDEFENMSVTRNSLNRDSDPPPARAQENGMPBE 120
Db 61 SIOPGAPKTIIVRSKSKAKOGALTLILDEFENMSVTRNSLNRDSDPPPARAQENGMPBE 120
QY 121 PATTAGGPGKAGSRFRFAGHSEAGGSGDRRRAGBEKPKSSREGSGGPOESSRDKRPL 180
Db 121 PATTAGGPGKAGSRFRFAGHSEAGGSGDRRRAGBEKPKSSREGSGGPOESSRDKRPL 180
QY 181 SGPDVGTPOPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPRDVA PNGPSAGLAIP 240
Db 181 SGPDVGTPOPAGLASGAKLAAGRPNTYPRADTDHPSRGAQGEPRDVA PNGPSAGLAIP 240
QY 241 QSSSSSSRPPTARAGAPSPGYLGPHASEPOLAPPACTPAPAPVPGPPGPRSPOREPORS 300
Db 241 QSSSSSSRPPTARAGAPSPGYLGPHASEPOLAPPACTPAPAPVPGPPGPRSPOREPORS 300
QY 301 HEQFPAALQLVYDPGDPBSYLDNFKIIGEGSTGIVCIATVRS SGKLVAVKMDLRKQORR 360
Db 301 HEQFPAALQLVYDPGDPBSYLDNFKIIGEGSTGIVCIATVRS SGKLVAVKMDLRKQORR 360
QY 361 ELLENEVVIMRDYOHENNVEMYSYLVGDELMVMEFLGGALTDI VTHTRANEQIAY 420
Db 361 ELLENEVVIMRDYOHENNVEMYSYLVGDELMVMEFLGGALTDI VTHTRANEQIAY 420
QY 421 CLAVLQALSVLAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTPY 480
Db 381 -----XLSDFGCAQVSKVPRRKSIVGTPY 406
QY 481 WMADELISRLEPYGEVDIWSLGIWIVEMVDEPPYENEPPLKAMKMI RDNLPRLNKLNK 540
Db 407 WMADELISRLEPYGEVDIWSLGIWIVEMVDEPPYENEPPLKAMKMI RDNLPRLNKLNK 466
QY 541 VSPSLKGFLDRLVDRDAQRATAELKHPFLAKAGPPASIVPLMRQNRTR 591
Db 467 VSPSLKGFLDRLVDRDAQRATAELKHPFLAKAGPPASIVPLMRQNRTR 517

Search completed: March 15, 2005, 11:26:30
Job time : 207.374 secs

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OM protein - protein search, using sw model

Run on: March 15, 2005, 11:30:37 ; Search time 160.787 Seconds
(without alignments)
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Title: US-10-693-367-2

Perfect score: 3090

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Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3090	100.0	591	US-09-291-417-103	Sequence 103, App
2	3090	100.0	591	US-10-134-102-4	Sequence 4, Appl
3	3090	100.0	591	US-10-394-322A-48	Sequence 48, Appl
4	3090	100.0	591	US-10-693-367-2	Sequence 2, Appl
5	3090	100.0	591	US-10-893-025-5	Sequence 5, Appl
6	3075	99.5	588	US-10-134-102-1	Sequence 1, Appl
7	2860	92.6	593	US-10-618-941-111	Sequence 11, App
8	2073	67.1	398	US-09-291-417-30	Sequence 30, Appl
9	1748	56.6	719	US-10-331-095-2	Sequence 2, Appl
10	1731	56.0	719	US-10-331-095-4	Sequence 4, Appl
11	1731	56.0	719	US-10-394-322A-49	Sequence 49, Appl
12	1502	48.6	292	US-10-406-676-5	Sequence 5, Appl
13	1502	48.6	292	US-10-406-676-6	Sequence 6, Appl

14	1502	48.6	292	US-10-406-676-8	Sequence 8, Appl
15	1502	48.6	292	US-10-406-676-9	Sequence 9, Appl
16	1502	48.6	292	US-10-406-676-10	Sequence 10, Appl
17	1502	48.6	292	US-10-406-676-11	Sequence 11, Appl
18	1502	48.6	292	US-10-406-676-12	Sequence 12, Appl
19	1497.5	48.5	639	US-10-406-676-4	Sequence 4, Appl
20	1494.5	48.4	635	US-10-134-102-6	Sequence 6, Appl
21	1481	47.9	292	US-10-134-102-2	Sequence 2, Appl
22	1481	47.9	292	US-10-406-676-7	Sequence 7, Appl
23	1473.5	47.7	681	US-10-406-676-12	Sequence 12, Appl
24	1470.5	47.6	681	US-09-291-417-29	Sequence 29, Appl
25	1421	46.0	292	US-09-765-815-2	Sequence 2, Appl
26	1335.5	43.2	641	US-10-406-676-15	Sequence 15, Appl
27	1303	42.2	290	US-10-311-034-15	Sequence 15, Appl
28	1289	41.7	290	US-10-406-676-13	Sequence 13, Appl
29	1289	41.7	290	US-10-406-676-14	Sequence 14, Appl
30	1289	41.7	290	US-10-406-676-16	Sequence 16, Appl
31	1277	41.3	290	US-10-406-676-17	Sequence 17, Appl
32	1213	39.3	290	US-10-693-367-3	Sequence 3, Appl
33	1209	39.1	290	US-10-406-676-18	Sequence 18, Appl
34	1209	39.1	290	US-10-406-676-19	Sequence 19, Appl
35	1147	37.1	292	US-10-406-676-20	Sequence 20, Appl
36	1096.5	35.5	540	US-10-406-676-21	Sequence 21, Appl
37	1090.5	35.3	542	US-10-369-493-6482	Sequence 6482, Ap
38	1024.5	33.2	580	US-10-369-493-6483	Sequence 6483, Ap
39	937.5	30.3	704	US-10-108-260A-3288	Sequence 3288, Ap
40	924	29.9	544	US-10-267-502-378	Sequence 378, App
41	909	29.4	544	US-10-267-502-382	Sequence 382, App
42	909	29.4	544	US-09-967-624-6	Sequence 6, Appl
43	909	29.4	544	US-10-289-161A-6	Sequence 6, Appl
44	909	29.4	544	US-10-394-322A-47	Sequence 47, Appl
45	909	29.4	544	US-10-267-502-379	Sequence 379, App
			544	US-10-757-262-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1	US-09-291-417-103	Sequence 103, Application US/09291417A
1	US-09-291-417-103	Sequence 103, Application US/09291417A
2	US-09-291-417-103	Sequence 103, Application US/09291417A
3	US-09-291-417-103	Sequence 103, Application US/09291417A
4	US-09-291-417-103	Sequence 103, Application US/09291417A
5	US-09-291-417-103	Sequence 103, Application US/09291417A
6	US-09-291-417-103	Sequence 103, Application US/09291417A
7	US-09-291-417-103	Sequence 103, Application US/09291417A
8	US-09-291-417-103	Sequence 103, Application US/09291417A
9	US-09-291-417-103	Sequence 103, Application US/09291417A
10	US-09-291-417-103	Sequence 103, Application US/09291417A
11	US-09-291-417-103	Sequence 103, Application US/09291417A
12	US-09-291-417-103	Sequence 103, Application US/09291417A
13	US-09-291-417-103	Sequence 103, Application US/09291417A
14	US-09-291-417-103	Sequence 103, Application US/09291417A
15	US-09-291-417-103	Sequence 103, Application US/09291417A
16	US-09-291-417-103	Sequence 103, Application US/09291417A
17	US-09-291-417-103	Sequence 103, Application US/09291417A
18	US-09-291-417-103	Sequence 103, Application US/09291417A
19	US-09-291-417-103	Sequence 103, Application US/09291417A
20	US-09-291-417-103	Sequence 103, Application US/09291417A
21	US-09-291-417-103	Sequence 103, Application US/09291417A
22	US-09-291-417-103	Sequence 103, Application US/09291417A
23	US-09-291-417-103	Sequence 103, Application US/09291417A
24	US-09-291-417-103	Sequence 103, Application US/09291417A
25	US-09-291-417-103	Sequence 103, Application US/09291417A
26	US-09-291-417-103	Sequence 103, Application US/09291417A
27	US-09-291-417-103	Sequence 103, Application US/09291417A
28	US-09-291-417-103	Sequence 103, Application US/09291417A
29	US-09-291-417-103	Sequence 103, Application US/09291417A
30	US-09-291-417-103	Sequence 103, Application US/09291417A
31	US-09-291-417-103	Sequence 103, Application US/09291417A
32	US-09-291-417-103	Sequence 103, Application US/09291417A
33	US-09-291-417-103	Sequence 103, Application US/09291417A
34	US-09-291-417-103	Sequence 103, Application US/09291417A
35	US-09-291-417-103	Sequence 103, Application US/09291417A
36	US-09-291-417-103	Sequence 103, Application US/09291417A
37	US-09-291-417-103	Sequence 103, Application US/09291417A
38	US-09-291-417-103	Sequence 103, Application US/09291417A
39	US-09-291-417-103	Sequence 103, Application US/09291417A
40	US-09-291-417-103	Sequence 103, Application US/09291417A
41	US-09-291-417-103	Sequence 103, Application US/09291417A
42	US-09-291-417-103	Sequence 103, Application US/09291417A
43	US-09-291-417-103	Sequence 103, Application US/09291417A
44	US-09-291-417-103	Sequence 103, Application US/09291417A
45	US-09-291-417-103	Sequence 103, Application US/09291417A

Db 121 PATTARGGPGKAGSRGPFAGHSEAGSGSDRRRAQPEKPKSRREGSGGQESSRDKRPL 180
QY 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
Db 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSRPPTARAGAPSPGVLPFAHSEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
Db 241 QSSSSSRPPTARAGAPSPGVLPFAHSEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 360
Db 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 360
QY 361 ELLENFVIMRDYQHENVEMNSYLVGDELVMVMELEGALTDIVTTRNNEQIAAV 420
Db 361 ELLENFVIMRDYQHENVEMNSYLVGDELVMVMELEGALTDIVTTRNNEQIAAV 420
QY 421 CLAVALSVLHAQVIRHDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVGTPI 480
Db 421 CLAVALSVLHAQVIRHDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVGTPI 480
QY 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYFNEPPLKAMKIRDNLPRLKNLHK 540
Db 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYFNEPPLKAMKIRDNLPRLKNLHK 540
QY 541 VSPSLKGFILDLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 591
Db 541 VSPSLKGFILDLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 591

RESULT 2
US-10-134-102-4
; Sequence 4, Application US/10134102
; Publication No. US20030186254A1
; GENERAL INFORMATION:
; APPLICANT: Weinick, Michael B.
; APPLICANT: Moritz, Albrecht
; APPLICANT: Comb, Michael J.
; TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
; FILE REFERENCE: CST-176 CIP
; CURRENT APPLICATION NUMBER: US/10/134,102
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/750,457
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/173,939
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-134-102-4

Query Match 100.0%; Score 3090; DB 14; Length 591;
Best Local Similarity 100.0%; Pred. No. 5,7e-161;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKVEISAPNFEHVRHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60
Db 1 MFGKRRKVEISAPNFEHVRHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60
QY 61 SIOPGAPKTIYRSGKAGDGLTLLDDEFENMSYTRNSLRRDPPPARARQENGMEEE 120
Db 61 SIOPGAPKTIYRSGKAGDGLTLLDDEFENMSYTRNSLRRDPPPARARQENGMEEE 120
QY 121 PATTARGGPGKAGSRGPFAGHSEAGSGSDRRRAQPEKPKSRREGSGGQESSRDKRPL 180
Db 121 PATTARGGPGKAGSRGPFAGHSEAGSGSDRRRAQPEKPKSRREGSGGQESSRDKRPL 180
QY 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240

Db 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSRPPTARAGAPSPGVLPFAHSEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
Db 241 QSSSSSRPPTARAGAPSPGVLPFAHSEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
QY 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 360
Db 301 HEQFRAALQLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 360
QY 361 ELLENFVIMRDYQHENVEMNSYLVGDELVMVMELEGALTDIVTTRNNEQIAAV 420
Db 361 ELLENFVIMRDYQHENVEMNSYLVGDELVMVMELEGALTDIVTTRNNEQIAAV 420
QY 421 CLAVALSVLHAQVIRHDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVGTPI 480
Db 421 CLAVALSVLHAQVIRHDIKSDSILLTHDGRVLSDFGCAQVSKVPRKSLVGTPI 480
QY 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYFNEPPLKAMKIRDNLPRLKNLHK 540
Db 481 WMAPELISRLPYGPEVDIWSLIGIMVTEMVDEBPYFNEPPLKAMKIRDNLPRLKNLHK 540
QY 541 VSPSLKGFILDLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 591
Db 541 VSPSLKGFILDLVDPDPRSYLDNFIKIGEGSTGICIAVTRSSGKLVAVKMDLRKQOR 591

RESULT 3
US-10-394-322A-48
; Sequence 48, Application US/10394322A
; Publication No. US2003023291A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-48

Query Match 100.0%; Score 3090; DB 15; Length 591;
Best Local Similarity 100.0%; Pred. No. 5,7e-161;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKVEISAPNFEHVRHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60
Db 1 MFGKRRKVEISAPNFEHVRHTGFDQHEQKFTGLPRQWOSLIESARRPKPLVDPACT 60
QY 61 SIOPGAPKTIYRSGKAGDGLTLLDDEFENMSYTRNSLRRDPPPARARQENGMEEE 120
Db 61 SIOPGAPKTIYRSGKAGDGLTLLDDEFENMSYTRNSLRRDPPPARARQENGMEEE 120
QY 121 PATTARGGPGKAGSRGPFAGHSEAGSGSDRRRAQPEKPKSRREGSGGQESSRDKRPL 180
Db 121 PATTARGGPGKAGSRGPFAGHSEAGSGSDRRRAQPEKPKSRREGSGGQESSRDKRPL 180
QY 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
Db 181 SGPDVGTPOPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVA PNGPSAGGLAIP 240
QY 241 QSSSSSRPPTARAGAPSPGVLPFAHSEPOLAPACTPAAPAVPGPPRSPQREPORVS 300
Db 241 QSSSSSRPPTARAGAPSPGVLPFAHSEPOLAPACTPAAPAVPGPPRSPQREPORVS 300

Qy	361	HEQFPAALQVLVDPGSPRSYLDNFIKIGGSGTICVIAIVRSSGKVLAVKMDLRQQR	360
Db	301	HEQFPAALQVLVDPGSPRSYLDNFIKIGGSGTICVIAIVRSSGKVLAVKMDLRQQR	360
Qy	361	ELLFNEVIMRDYQEHENVEMNYSYVGBELVMNVEFEGGALTDIVTTHRNNEBOIAAV	420
Db	361	ELLFNEVIMRDYQEHENVEMNYSYVGBELVMNVEFEGGALTDIVTTHRNNEBOIAAV	420
Qy	421	CLAVIQALSYLHAQGVYIHRDICKSDSTLLPHDGRVKLSDFGCQAVSKEVPRRSKLVGTPY	480
Db	421	CLAVIQALSYLHAQGVYIHRDICKSDSTLLPHDGRVKLSDFGCQAVSKEVPRRSKLVGTPY	480
Qy	481	WMAPELISRLPYGPEVDIWSLGIWVEMWDGEPPEYNEBPPLKAMKMIKMDLPRLLNHLK	540
Db	481	WMAPELISRLPYGPEVDIWSLGIWVEMWDGEPPEYNEBPPLKAMKMIKMDLPRLLNHLK	540
Qy	541	VSPSLKGFLLVDRDPORATPAELIKKHPFLAKAGPPASIVLMMONTR	591
Db	541	VSPSLKGFLLVDRDPORATPAELIKKHPFLAKAGPPASIVLMMONTR	591

RESULT 4
US-10-693-367-2

```

: Sequence 2, Application US/10693367
: Publication No. US20040091992A1
:
: GENERAL INFORMATION:
:
: APPLICANT: The Trustees of Columbia University
: APPLICANT: Minden, Audrey
:
: TITLE OF INVENTION: PK4, A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
: FILE REFERENCE: 575/55311-A-PCT-US
: CURRENT APPLICATION NUMBER: US/10/693,367
: CURRENT FILING DATE: 2003-10-24
: PRIOR APPLICATION NUMBER: US/09/718,032
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: PCT/US99/11341
: PRIOR FILING DATE: 1999-05-21
: PRIOR APPLICATION NUMBER: 09/082,737
: PRIOR FILING DATE: 1998-05-21
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn version 3.1
:
: SEQ ID NO 2
:
: LENGTH: 591
:
: TYPE: PRT
:
: ORGANISM: human
:
: US-10-693-367-2

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Query Match	100.0%;	Score 3090;	DB 15;	length 591;
Best Local Similarity	100.0%;	Pred. No. 5.7e-161;		
Matches 591;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MEGKKKREIAPSNFIEHRVHTGFOHQKFLGRLROMQSLIEESARRKPLVDPACIT	60
Db	1	MEGKKKKVEISAPSNFIEHRVHTGFOHQKFLGRLROMQSLIEESARRKPLVDPACIT	60
QY	61	SIQPGAPRTIYVSGSKAKDGALTLLIDEFBNNSVTNSILRRDSPPPPARARQENMPPEE	120
Db	61	SIQPGAPRTIYVSGSKAKDGALTLLIDEFBNNSVTNSILRRDSPPPPARARQENMPPEE	120
QY	121	PATTARGGPKGKSGRCRPFAGHSEAGGSGDRRRAGCEPKPKSREBSGGQOESSRDKRPL	180
Db	121	PATTARGGPKGKSGRCRPFAGHSEAGGSGDRRRAGCEPKPKSREBSGGQOESSRDKRPL	180
QY	181	SGPDVGTPOPAGLASGAKLAAGRPFNTYTPAULTDHPSRGAQGEPPHYAPNGPSAGGLATP	240
Db	181	SGPDVGTPOPAGLASGAKLAAGRPFNTYTPAULTDHPSRGAQGEPPHYAPNGPSAGGLATP	240
QY	241	QSSSSSSRPRTARCAPSPGVLCPHASEPOLAPACTPAAPAVAPGPPGPSPOREQRVS	300
Db	241	QSSSSSSRPRTARCAPSPGVLCPHASEPOLAPACTPAAPAVAPGPPGPSPOREQRVS	300
QY	301	HEQFPALALVYDQDPRSYLDFIKIGBSTGIVCIATYRSSGKLVAYKKMLRKCQRR	360
Db	301	HEQFPALALVYDQDPRSYLDFIKIGBSTGIVCIATYRSSGKLVAYKKMLRKCQRR	360

QY	361	ELLFEEVIMADYOHENNVEMNSVLGBELVWMEFLEGGLTIDVTITRNNEEOIAAV	420
Db	361	ELLFEEVIMADYOHENNVEMNSVLGBELVWMEFLEGGLTIDVTITRNNEEOIAAV	420
QY	421	CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKLVGTPY	480
Db	421	CLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKLVGTPY	480
QY	481	WMAPPLISRLPYGPEVDIWSLGIWITIEWMDGPPYFNEPPLKAMKQIIRNLPRLLNLHK	540
Db	481	WMAPPLISRLPYGPEVDIWSLGIWITIEWMDGPPYFNEPPLKAMKQIIRNLPRLLNLHK	540
QY	541	VSPSLKGFDLRLVADPAORATAAEILKAPFLAKKGPSPASIVPLMRQNRTR	591
Db	541	VSPSLKGFDLRLVADPAORATAAEILKAPFLAKKGPSPASIVPLMRQNRTR	591

RESULT 5
US-10-85

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Sequence 5, Application US/10893025,
Publication No. US20050037965A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharma Deutschland GmbH
APPLICANT: BARRADEAU, Sebastien
APPLICANT: BARTNIK, Eckart
APPLICANT: CZECH, Joerg
APPLICANT: BLATT, Andreas
APPLICANT: LEBERER, Ekkehard
APPLICANT: LEEUW, Thomas
TITLE OF INVENTION: Use of a PAK inhibitor for the Treatment of a Joint Disease
FILE REFERENCE: DE4V2003/0055 US NP
CURRENT APPLICATION NUMBER: US/10/893,025
CURRENT FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: 60/527,819
PRIOR FILING DATE: 2003-12-08
PRIOR APPLICATION NUMBER: 03016306.4
PRIOR FILING DATE: 2004-07-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 591
TYPE: PRT
ORGANISM: Homo sapiens
US-10-893-025-5

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Query Match	100.0%;	Score 3090;	DB 17;	Length 591;
Best Local Similarity	100.0%;	Pred. No. 5.7e-161;		
Matches 591;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MEGRKKKVEISAPNFEHRVHTGDQHOEOKRTGTGLPRQOSIIEESARRPKPLVDPACIT	60
Db	1	MEGRKKKVEISAPNFEHRVHTGDQHOEOKRTGTGLPRQOSIIEESARRPKPLVDPACIT	60
QY	61	SIQBPAPRTIYRSGSKAGDGLATLLIDEEFNMSVYRNSLRKDSPPPAPARQENMPPEE	120
Db	61	SIQBPAPRTIYRSGSKAGDGLATLLIDEEFNMSVYRNSLRKDSPPPAPARQENMPPEE	120
QY	121	PATTARGGPGKAGSRGRFAGHSEAGGSGSDRRRAGCEKSPKSRREGSGGPOESSRDKRPL	180
Db	121	PATTARGGPGKAGSRGRFAGHSEAGGSGSDRRRAGCEKSPKSRREGSGGPOESSRDKRPL	180
QY	161	SGPDVGTGTPAGLAGATLAAGRPRNTYTRADTHDPSRCAQEPHHVAPNPGPAGGLAIP	240
Db	161	SGPDVGTGTPAGLAGATLAAGRPRNTYTRADTHDPSRCAQEPHHVAPNPGPAGGLAIP	240
QY	241	QSSSSSSRPPTARCAPSPBGVLGPHASBEQOLAPACTPAAPAVPGPGRSPQREBORVS	300
Db	241	QSSSSSSRPPTARCAPSPBGVLGPHASBEQOLAPACTPAAPAVPGPGRSPQREBORVS	300
QY	301	HEQFPAAAIQLVDPEDPRSGLDNFKLIGGSGTGYCIATVRSSGKVAWKMDLRQOQR	360
Db	301	HEQFPAAAIQLVDPEDPRSGLDNFKLIGGSGTGYCIATVRSSGKVAWKMDLRQOQR	360

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QY 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLGALTDIVTHTRMNEBOIAAV 420
DB 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLGALTDIVTHTRMNEBOIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPY 480
DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPY 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWYEMWDGEPYPFNEPPLKAMKIRDNLPRLKXJLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWYEMWDGEPYPFNEPPLKAMKIRDNLPRLKXJLHK 540
QY 541 VSPSLKGFIDRLVDPDPAQRATAAELKHPLAKGPPASIVPLMRONR 591
DB 541 VSPSLKGFIDRLVDPDPAQRATAAELKHPLAKGPPASIVPLMRONR 591

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RESULT 6

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US-10-134-102-1
/ Sequence 1, Application US/10134102
/ Publication No. US20030186254A1
/ GENERAL INFORMATION:
/ APPLICANT: Melnick, Michael B.
/ APPLICANT: Moritz, Albrecht
/ APPLICANT: Comb, Michael J.
/ TITLE OF INVENTION: Regulation of HIV-Tat and Nef by the Pak4 kinase and its
/ FILE REFERENCE: CST-176 CIP
/ CURRENT APPLICATION NUMBER: US/10/134,102
/ PRIOR FILING DATE: 2002-04-29
/ PRIOR APPLICATION NUMBER: 09/750,457
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: 60/173,939
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 588
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-134-102-1

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Query Match 99.5%; Score 3075; DB 14; Length 588;
Best Local Similarity 100.0%; Pred. No. 3,7e-160;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MFGKRRKRVISAPSNFHRVHTGPDQHKFTGLPRQWOSLIESARPKPLVDPACIT 60
DB 1 MFGKRRKRVISAPSNFHRVHTGPDQHKFTGLPRQWOSLIESARPKPLVDPACIT 60
QY 61 SIOPGAPKTIIVSGSKAGDGAULTLLDEFENMSVTRNSLRDSDPPPARARQENGMBEE 120
DB 61 SIOPGAPKTIIVSGSKAGDGAULTLLDEFENMSVTRNSLRDSDPPPARARQENGMBEE 120
QY 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKPKSREGSGGPOESSRDRPL 180
DB 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKPKSREGSGGPOESSRDRPL 180
QY 181 SGPDVGTQPPAGLGAAGLAAAGRPNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
DB 181 SGPDVGTQPPAGLGAAGLAAAGRPNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
QY 241 QSSSSSSRPPTARAGAPSPGVLCFPHASEPOLAPACTPAAPAVGPPGPPSPQREPORS 300
DB 241 QSSSSSSRPPTARAGAPSPGVLCFPHASEPOLAPACTPAAPAVGPPGPPSPQREPORS 300
QY 301 HEQFPAALQVLVDPDPRSVDNFYIKIGEGSTGIVCIATVRSSGKLVAAVKMDLRKQOR 360
DB 301 HEQFPAALQVLVDPDPRSVDNFYIKIGEGSTGIVCIATVRSSGKLVAAVKMDLRKQOR 360
QY 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLGALTDIVTHTRMNEBOIAAV 420

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DB 361 ELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLGALTDIVTHTRMNEBOIAAV 420
QY 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPY 480
DB 421 CLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVGTPY 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWYEMWDGEPYPFNEPPLKAMKIRDNLPRLKXJLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWYEMWDGEPYPFNEPPLKAMKIRDNLPRLKXJLHK 540
QY 541 VSPSLKGFIDRLVDPDPAQRATAAELKHPLAKGPPASIVPLMRON 588
DB 541 VSPSLKGFIDRLVDPDPAQRATAAELKHPLAKGPPASIVPLMRON 588

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RESULT 7

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US-10-618-941-111
/ Sequence 111, Application US/10618941
/ Publication No. US2004019792A1
/ GENERAL INFORMATION:
/ APPLICANT: WHYTE, DAVID
/ APPLICANT: MANNING, GERARD
/ APPLICANT: CAENEPEEL, SEAN
/ TITLE OF INVENTION: NOVEL KINASES
/ FILE REFERENCE: 034536-0321
/ CURRENT APPLICATION NUMBER: US/10/618,941
/ PRIOR FILING DATE: 2003-07-15
/ PRIOR APPLICATION NUMBER: 60/355,632
/ NUMBER OF SEQ ID NOS: 143
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 111
/ LENGTH: 593
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-618-941-111

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Query Match 92.6%; Score 2860; DB 16; Length 593;
Best Local Similarity 92.6%; Pred. No. 2,1e-148;
Matches 550; Conservative 10; Mismatches 30; Indels 4; Gaps 2;

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QY 1 MFGKRRKRVISAPSNFHRVHTGPDQHKFTGLPRQWOSLIESARPKPLVDPACIT 60
DB 1 MFGKRRKRVISAPSNFHRVHTGPDQHKFTGLPRQWOSLIESARPKPLVDPACIT 60
QY 61 SIOPGAPKTIIVSGSKAGDGAULTLLDEFENMSVTRNSLRDSDPPPARARQENGMBEE 120
DB 61 SIOPGAPKTIIVSGSKAGDGAULTLLDEFENMSVTRNSLRDSDPPPARARQENGMBEE 120
QY 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKPKSREGSGGPOESSRDRPL 180
DB 121 PATTAGGCGKAGSKRRFAGHSEAGGSGDRRRAPPEKPKSREGSGGPOESSRDRPL 180
QY 181 SGPDVGTQPPAGLGAAGLAAAGRPNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
DB 181 SGPDVGTQPPAGLGAAGLAAAGRPNTYPRADTHPSRGAQGEPHDVAEPNGPSAGLAI 240
QY 241 QSSSSSSRPPTARAGAPSPGVLCFPHASEPOLAPACTPAAPAVGPPGPPSPQREPORS 297
DB 241 QSSSSSSRPPTARAGAPSPGVLCFPHASEPOLAPACTPAAPAVGPPGPPSPQREPORS 297
QY 298 RVSHQFPAALQVLVDPDPRSVDNFYIKIGEGSTGIVCIATVRSSGKLVAAVKMDLRKQ 357
DB 298 RVSHQFPAALQVLVDPDPRSVDNFYIKIGEGSTGIVCIATVRSSGKLVAAVKMDLRKQ 357
QY 358 QRRBELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLGALTDIVTHTRMNEBOIAAV 417
DB 358 QRRBELLENVIMRDYQHENVVEMNSYLVGDELWVMEFLGALTDIVTHTRMNEBOIAAV 417
QY 418 AAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVG 477
DB 420 AAVCLAVLQALSVLHAQGVTHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRKRSIVG 479

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QY 478 TPYMAPELISRLPYGEVDINSLGIMVEMVDEBPYNEPPLKAMKIMRDLPRLLKN 537
DB 480 TPYMAPELISRLPYGEVDINSLGIMVEMVDEBPYNEPPLKAMKIMRDLPRLLKN 539
QY 538 LHKVPSLKGFLDLRLVRDPACRATAEELKHPEFLAKAGPPASIVPLMQRNTR 591
DB 540 LHKASPSLKGFLDLRLVRDPACRATAEELKHPEFLAKAGPPASIVPLMQRNTR 593

RESULT 8
US-09-291-417-30

; Sequence 30, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MYHRE, DAVID
; TITLE OF INVENTION: STEZO-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT FILING DATE: US/09/291,417A
; EARLIER FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mammalian (Human) PAK5
US-09-291-417-30

Query Match 67.1%; Score 2073; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.4e-105;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPPAGGLAIPOSSSSSRPPTTA 253
DB 1 ASAKLAAGRPFTYPRADTDHPSRGAQGEPHDVAENGPPAGGLAIPOSSSSSRPPTTA 60
QY 254 RGAPEGVIGPHASEPQALAPACTPAAPAVPGPPGPRSPQREPORVSHQFRAALQVVD 313
DB 61 RGAPEGVIGPHASEPQALAPACTPAAPAVPGPPGPRSPQREPORVSHQFRAALQVVD 120
QY 314 PGDPRLYDNFIKIGSGTIGVCIATVRSSGKLVAAKMDLRKQORRELLFNEVIMRDY 373
DB 121 PGDPRLYDNFIKIGSGTIGVCIATVRSSGKLVAAKMDLRKQORRELLFNEVIMRDY 180
QY 374 QHENNVEMNSYVGEELWVMEFLGALTDIVTTRMGEQIAVCLAVLQALSVLHA 433
DB 181 QHENNVEMNSYVGEELWVMEFLGALTDIVTTRMGEQIAVCLAVLQALSVLHA 240
QY 434 QGVYHDKISDILTLTHDGRVKLSDFGCAQVSKEVPARRKSLVGTPTYMAPELISRLPYG 493
DB 241 QGVYHDKISDILTLTHDGRVKLSDFGCAQVSKEVPARRKSLVGTPTYMAPELISRLPYG 300
QY 494 PEVDISLGIWIEVMDGEPYNEPPLKAMKIMRDLPRLLKHLKVSPLKGLDRL 553
DB 301 PEVDISLGIWIEVMDGEPYNEPPLKAMKIMRDLPRLLKHLKVSPLKGLDRL 360
QY 554 VRDPACRATAEELKHPEFLAKAGPPASIVPLMQRNTR 591
DB 361 VRDPACRATAEELKHPEFLAKAGPPASIVPLMQRNTR 398

RESULT 9
US-10-331-095-2

; Sequence 2, Application US/10331095
; Publication No. US20030124107A1
; GENERAL INFORMATION:
; APPLICANT: Columbia University
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK5-Related Compositions and Methods
; FILE REFERENCE: 0575/64083-A

; CURRENT APPLICATION NUMBER: US/10/331,095
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/343,972
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: mouse PAK5
US-10-331-095-2

Query Match 56.6%; Score 1748; DB 14; Length 719;
Best Local Similarity 52.9%; Pred. No. 1.4e-87;
Matches 385; Conservative 65; Mismatches 128; Indels 150; Gaps 16;

QY 1 MFGRKKRVEIGAPSNFEHRYHTTGPQHOKFTTGLPRQWOSLIEBARRPKLVDPACTT 60
DB 1 MFGRKKRVEIGAPSNFEHRYHTTGPQHOKFTTGLPRQWOSLIEBARRPKLVDPACTT 60
QY 61 STOPGAPKTIYVSGSKADGALTLLDEPEFNNVYTRSNLSRRDSPPP---AAR----- 112
DB 61 PIQAPMKTIYVSGSKADGALTLLDEPEFNNVYTRSNLSRRDSPPP---AAR----- 120
QY 113 QENGM-----DEEPATTARGGPRKAGSRGPA-----GH----- 141
DB 121 EENGFITFGQYSSSDTTADYTTTEKYRDRSLVGDLDLYKSSHAQKNGHAMKMGHDA 180
QY 142 -----SEAGGSGDPRRA----- 154
DB 181 YYPEMKSIXTLADGPEVDYHTHLSLRKSEYGLRMDYQRASSSPLDYSFQLTPSRTA 240
QY 155 -----GP-----EKRPKSSREGSGQPQESSRDKRPLSGPDVGP-OPA 191
DB 241 GHSRCKESLAVSESNWGSLLDYPDRPKSSYLHQTSFPPAKR-QKSGSGSLGQEMMF 299
QY 192 GLASGAKLAAGRPFTY-----PRADTDH-----PSRGAQGEPHDVAENG 232
DB 300 GASAFKTHPQHSYNSYTYPRLSSEPTMCI PKYDYDRAQVVFSPPLSGS-----DTYPRGP 354
QY 233 SAGGLAIPOS-----SSSSSRPPTRAGA-----PSPEVLGPHASEPQALAPACTPAAP 281
DB 355 T-----KLPOSQKAGYSSGSHQYPSGYNHRAVDYHNSLQTSQY1STASYL-SSLSISS 409
QY 282 AVPGPPGPRSPQREPORVSHQFRAALQVVDPGDPRLYDNFIKIGSGTIGVCIATYR 341
DB 410 TYPPESWSSSDQQEPKRVSHQFRAALQVVDPGDPRLYDNFIKIGSGTIGVCIATYR 469
QY 342 SSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENNVEMNSYVGEELWVMEFLGEG 401
DB 470 HNGKQVAAVKMDLRKQORRELLFNEVIMRDYQHENNVEMNSYVGEELWVMEFLGEG 529
QY 402 ALTDIVTTRMGEQIAVCLAVLQALSVLHAQGVYHDKISDILTLTHDGRVKLSDFG 461
DB 530 ALTDIVTTRMGEQIAVCLAVLQALSVLHAQGVYHDKISDILTLTHDGRVKLSDFG 589
QY 462 CAQVSKEVPARRKSLVGTPTYMAPELISRLPYGEVDINSLGIMVEMVDEBPYNEPPL 521
DB 590 CAQVSKEVPARRKSLVGTPTYMAPELISRLPYGEVDINSLGIMVEMVDEBPYNEPPL 649
QY 522 KAMKIMRDLPRLLKHLKVSPLKGLDRLVRDPACRATAEELKHPEFLAKAGPPASI 581
DB 650 QAMBRIRDSLPRVVDLHKVSSWLGFLDMLVREPSQATQOELLGHFPLKLAGPPSCI 709
QY 582 VPLMQRNTR 589
DB 710 VPLMQRNTR 717

RESULT 10

US-10-331-095-4
 ; Sequence 4, Application US/10331095
 ; Publication No. US20030124107A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Columbia University
 ; APPLICANT: Wanden, Audrey
 ; TITLE OF INVENTION: PAKS-Related Compositions and Methods
 ; FILE REFERENCE: 0575/64083-A
 ; CURRENT APPLICATION NUMBER: US/10/331,095
 ; PRIOR FILING DATE: 2002-12-27
 ; PRIOR APPLICATION NUMBER: 60/343,972
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 719
 ; TYPE: PRT
 ; ORGANISM: human
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; OTHER INFORMATION: Human PAKS
 US-10-331-095-4

Query Match 56.0%; Score 1731; DB 14; Length 719;
 Best Local Similarity 52.4%; Pred. No. 1,2e-86;
 Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKRRKVEISAPSNFEHRVHTGPDHOKFTGLPRQMSLIESARRPKPLVDPACT 60
 DB 1 MFGKKKKKIRISGNSFNEHRVHTGPDHOKFTGLPRQMSLADTANRPKPKVNDSCIT 60
 QY 61 SIQGPARTIVRSGKAKDGLTLTLDDEFENMSTNSLRDSDPPPARA-----R 112
 DB 61 PIQAPKTIIVRGNKPKCKETSINGLEDPNISVTRNSLRKESPTPOQASGSHGPHA 120
 QY 113 QENGM-----PREPATA-----RG-----PGKA 132
 DB 121 EENGFITFSQYSSSDTADYTTEKYREKSLYGDDLDPRYKSHAKONGHVMKMGHEA 180
 QY 133 -----GSRGPAGH-----SEAG 145
 DB 181 YSEVVKPLKSDPARFADYHSHLDSLSKPEYSDLMKEYORASSSPLDYSFOFTPSRTA 240
 QY 146 GSGGDRRA-----GP-----EKRPKSRSGSGPOESSRDKRPLSGDVGTG-OPA 191
 DB 241 GTSKCSKESLAVSESEWGPGLDDYDRPKSYLNOTSPQPTMR-QRSRSGSLQEPMPMF 299
 QY 192 GLASGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEPHDVAFNGP 232
 DB 300 GASAFKTHPOGHSYNSYTYPRLSPTMCI PKVDYDRAQMVLSPLSGS-----DTYRGP 354
 QY 233 SAGGLAIPOS-----SSSSSRPPTRARGAPSPVLGPHASEPOLAPACTP----- 278
 DB 355 A-----TLPOSGSKSGYSSSSHQYPSGYNKA-----TLYHNPISLOSSQYISTASYLSISL 406
 QY 279 AARAVGPPGPRSPORFORSVSHQFRAALQLVDPDPSPSYLDNFIKIGESTGIYCIA 338
 DB 407 SSSYTPPSPWSSSDQOPSRVSHQFRAALQLVSPDPSPREYLANFIKIGESTGIYCIA 466
 QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVEMYNSTLVGDELVMVMEFL 398
 DB 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVEMYNSTLVGDELVMVMEFL 526
 QY 399 EGGLALTDIVTTRNNEBOIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLS 458
 DB 527 EGGLALTDIVTTRNNEBOIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLS 586
 QY 459 FGFCQAVSKEVPRRKSIVGTPTPYMAPELISRLPYGPEVDIWSIGIWMVDEPPYFNE 518
 DB 587 FGFCQAVSKEVPRRKSIVGTPTPYMAPELISRLPYGPEVDIWSIGIWMVDEPPYFNE 646
 QY 519 PPLQAMKIRIDSLPRVKDLHKVSVLRGFLDMLVREPSORATAQELLGHPFLKLAGPP 578

DB 647 PPLQAMKIRIDSLPRVKDLHKVSVLRGFLDMLVREPSORATAQELLGHPFLKLAGPP 706
 QY 579 ASIVPLMRQNR 589
 DB 707 SCIVPLMRQYR 717

RESULT 11
 US-10-394-322A-49
 ; Sequence 49, Application US/10394322A
 ; Publication No. US20030232391A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
 ; APPLICANT: Prescott, John C.
 ; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
 ; FILE REFERENCE: 39750-0006 US
 ; CURRENT APPLICATION NUMBER: US/10/394,322A
 ; PRIOR FILING DATE: 2003-03-20
 ; PRIOR APPLICATION NUMBER: US 60/366,892
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PaetSeq for Windows Version 4.0
 ; SEQ ID NO 49
 ; LENGTH: 719
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-394-322A-49

Query Match 56.0%; Score 1731; DB 15; Length 719;
 Best Local Similarity 52.4%; Pred. No. 1,2e-86;
 Matches 383; Conservative 66; Mismatches 126; Indels 156; Gaps 17;

QY 1 MFGKRRKVEISAPSNFEHRVHTGPDHOKFTGLPRQMSLIESARRPKPLVDPACT 60
 DB 1 MFGKKKKKIRISGNSFNEHRVHTGPDHOKFTGLPRQMSLADTANRPKPKVNDSCIT 60
 QY 61 SIQGPARTIVRSGKAKDGLTLTLDDEFENMSTNSLRDSDPPPARA-----R 112
 DB 61 PIQAPKTIIVRGNKPKCKETSINGLEDPNISVTRNSLRKESPTPOQASGSHGPHA 120
 QY 113 QENGM-----PREPATA-----RG-----PGKA 132
 DB 121 EENGFITFSQYSSSDTADYTTEKYREKSLYGDDLDPRYKSHAKONGHVMKMGHEA 180
 QY 133 -----GSRGPAGH-----SEAG 145
 DB 181 YSEVVKPLKSDPARFADYHSHLDSLSKPEYSDLMKEYORASSSPLDYSFOFTPSRTA 240
 QY 146 GSGGDRRA-----GP-----EKRPKSRSGSGPOESSRDKRPLSGDVGTG-OPA 191
 DB 241 GTSKCSKESLAVSESEWGPGLDDYDRPKSYLNOTSPQPTMR-QRSRSGSLQEPMPMF 299
 QY 192 GLASGAKLAAGRPNTY-----PRADTDH-----PSRGAQGEPHDVAFNGP 232
 DB 300 GASAFKTHPOGHSYNSYTYPRLSPTMCI PKVDYDRAQMVLSPLSGS-----DTYRGP 354
 QY 233 SAGGLAIPOS-----SSSSSRPPTRARGAPSPVLGPHASEPOLAPACTP----- 278
 DB 355 A-----TLPOSGSKSGYSSSSHQYPSGYNKA-----TLYHNPISLOSSQYISTASYLSISL 406
 QY 279 AARAVGPPGPRSPORFORSVSHQFRAALQLVDPDPSPSYLDNFIKIGESTGIYCIA 338
 DB 407 SSSYTPPSPWSSSDQOPSRVSHQFRAALQLVSPDPSPREYLANFIKIGESTGIYCIA 466
 QY 339 TVRSSGKLVAVKMDLRKQORRELLFNEVIMRDYQHENVEMYNSTLVGDELVMVMEFL 398
 DB 467 TEKHTGKQVAVKMDLRKQORRELLFNEVIMRDYQHENVEMYNSTLVGDELVMVMEFL 526
 QY 399 EGGLALTDIVTTRNNEBOIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLS 458
 DB 527 EGGLALTDIVTTRNNEBOIAVCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYKLS 586
 QY 459 FGFCQAVSKEVPRRKSIVGTPTPYMAPELISRLPYGPEVDIWSIGIWMVDEPPYFNE 518


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Db      587  FEGCAQVSKEVPRKSLVGPYMAAEVSRLLPYGHEVDIMSLGIVIMIDSEPPYFHE 646
        519  PPLKAMKMTIDNLPPLKMLHKVSPSLKGFLLVDPAPORATTAELLKHPFLAYAGPP 578
        647  PPLQAMRRIRDSIPPRVKDLHKVSVLRGFLDMLVREPSQRATAELLGHPFLKLAGPP 706
Qy      579  ASIVPLMRQNR 589
        707  SCTIVPLMRQYR 717

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RESULT 12

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US-10-406-676-5
/ Sequence 5, Application US/10406676
/ Publication No. US20030229453A1
/ GENERAL INFORMATION:
/ APPLICANT: Structural Genomix, Inc.
/ APPLICANT: Anthonyamy, Stephen
/ APPLICANT: Fell, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-406-676-5

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Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      300  SHEQFRAALQLVVDPPDPSYLDNFKIGEGSTGIVCIATVRSSGKLVAVKMDLKKQOR 359
        1  SHEQFRAALQLVVDPPDPSYLDNFKIGEGSTGIVCIATVRSSGKLVAVKMDLKKQOR 60
Db      360  RELLFNEVYIMRDYQHEHVENYNSYLVDDELVMVMEFEGGALTDIVHTTRMNEQIAA 419
        61  RELLFNEVYIMRDYQHEHVENYNSYLVDDELVMVMEFEGGALTDIVHTTRMNEQIAA 120
Qy      420  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVPRKSLVGRP 479
        121  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVPRKSLVGRP 180
Db      480  YMAAPELISRLPYGPEVDIWSLGINVIEVNDGEPFYFNEBPPLKAMKMTIDNLPPLKNTLH 539
        181  YMAAPELISRLPYGPEVDIWSLGINVIEVNDGEPFYFNEBPPLKAMKMTIDNLPPLKNTLH 240
Qy      540  KVSPLSKGFLDLVLVDPAPORATTAELLKHPFLAKGPPASIVPLMRQNR 591
        241  KVSPLSKGFLDLVLVDPAPORATTAELLKHPFLAKGPPASIVPLMRQNR 292
Db

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RESULT 13

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US-10-406-676-6
/ Sequence 6, Application US/10406676
/ Publication No. US20030229453A1
/ GENERAL INFORMATION:
/ APPLICANT: Structural Genomix, Inc.
/ APPLICANT: Anthonyamy, Stephen

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/ APPLICANT: Fell, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-406-676-6

```

```

Query Match      48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      300  SHEQFRAALQLVVDPPDPSYLDNFKIGEGSTGIVCIATVRSSGKLVAVKMDLKKQOR 359
        1  SHEQFRAALQLVVDPPDPSYLDNFKIGEGSTGIVCIATVRSSGKLVAVKMDLKKQOR 60
Db      360  RELLFNEVYIMRDYQHEHVENYNSYLVDDELVMVMEFEGGALTDIVHTTRMNEQIAA 419
        61  RELLFNEVYIMRDYQHEHVENYNSYLVDDELVMVMEFEGGALTDIVHTTRMNEQIAA 120
Qy      420  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVPRKSLVGRP 479
        121  VCLAVLQALSVLHAQGVIRHDIKSDSILLTHDGRVYLSDFGCAQVSKVPRKSLVGRP 180
Db      480  YMAAPELISRLPYGPEVDIWSLGINVIEVNDGEPFYFNEBPPLKAMKMTIDNLPPLKNTLH 539
        181  YMAAPELISRLPYGPEVDIWSLGINVIEVNDGEPFYFNEBPPLKAMKMTIDNLPPLKNTLH 240
Qy      540  KVSPLSKGFLDLVLVDPAPORATTAELLKHPFLAKGPPASIVPLMRQNR 591
        241  KVSPLSKGFLDLVLVDPAPORATTAELLKHPFLAKGPPASIVPLMRQNR 292
Db

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RESULT 14

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US-10-406-676-8
/ Sequence 8, Application US/10406676
/ Publication No. US20030229453A1
/ GENERAL INFORMATION:
/ APPLICANT: Structural Genomix, Inc.
/ APPLICANT: Anthonyamy, Stephen
/ APPLICANT: Fell, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 292
/ TYPE: PRT

```

/ ORGANISM: H.sapiens
US-10-406-676-8

Query Match 48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEOPRALQLVDPGPRSYLDFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQOR 359
DB 1 SHEOPRALQLVDPGPRSYLDFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQOR 60
QY 360 RELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEEQIAA 419
DB 61 RELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEEQIAA 120
QY 420 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTP 479
DB 121 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTP 180
QY 480 YMAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 539
DB 181 YMAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 240
QY 540 KVSPLKGFILDRLLVRDPAQRATAELLKHPLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSPLKGFILDRLLVRDPAQRATAELLKHPLAKAGPPASIVPLMRQNRTR 292

RESULT 15

US-10-406-676-9
/ Sequence 9, Application US/10406676
/ Publication No. US20030229453A1
/ GENERAL INFORMATION:
/ APPLICANT: Structural Genomix, Inc.
/ APPLICANT: Antonysamy, Stephen
/ APPLICANT: Feil, Ingeborg
/ APPLICANT: Buchanan, Sean
/ APPLICANT: Post, Kai W.
/ APPLICANT: Liu, Yi
/ APPLICANT: Lorber, David
/ TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF PAK4KD KINASE
/ FILE REFERENCE: 524982002300
/ CURRENT APPLICATION NUMBER: US/10/406,676
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/371,018
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/430,567
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: H.sapiens
US-10-406-676-9

Query Match 48.6%; Score 1502; DB 15; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 SHEOPRALQLVDPGPRSYLDFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQOR 359
DB 1 SHEOPRALQLVDPGPRSYLDFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQOR 60
QY 360 RELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEEQIAA 419
DB 61 RELLFNEVIMRDYQHENVVEMVNSYLVGDELWVMEFLGALTDIVTHTRMNEEQIAA 120
QY 420 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTP 479
DB 121 VCLAVLQALSVLHAGVYIHRDIKSDSILLTHDGRVKLSDFGCAQVSKVPRRKSIVGTP 180

QY 480 YMAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 539
DB 181 YMAPELISRLPYGPEVDIWSLGIWVIEWVDGEPYFNEPPLKAMKMIKRDNLPRRLKNLH 240
QY 540 KVSPLKGFILDRLLVRDPAQRATAELLKHPLAKAGPPASIVPLMRQNRTR 591
DB 241 KVSPLKGFILDRLLVRDPAQRATAELLKHPLAKAGPPASIVPLMRQNRTR 292

Search completed: March 15, 2005, 11:47:58
Job time : 162.787 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 11:18:02 ; Search time 52.1471 Seconds

(without alignments)
846.023 Million cell updates/sec

Title: US-10-693-367-2

Perfect score: 3090

Sequence: 1 MGKRRKRVETISAPSNFEHR.....LAKAGPASIPLMQRNR 591

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:.*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:.*
4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3090	100.0	591	3	US-09-082-737-2
2	3090	100.0	591	4	US-09-688-188B-103
3	3090	100.0	591	4	US-09-718-032-2
4	3090	100.0	591	4	US-09-291-417D-103
5	3090	100.0	591	4	US-09-949-016-6665
6	3090	100.0	620	4	US-09-949-016-7206
7	2073	67.1	398	4	US-09-688-188B-30
8	2073	67.1	398	4	US-09-291-417D-30
9	1473.5	47.7	681	4	US-09-688-188B-29
10	1473.5	47.7	681	4	US-09-291-417D-29
11	1473.5	47.7	694	4	US-09-949-016-10445
12	1470.5	47.6	681	4	US-09-765-815-2
13	1277	41.3	250	3	US-09-082-737-3
14	1277	41.3	250	4	US-09-718-032-3
15	912	29.5	544	2	US-08-935-760-2
16	909	29.4	544	4	US-09-949-016-11562
17	907	29.4	544	4	US-09-688-188B-95
18	907	29.4	544	4	US-09-291-417D-95
19	904	29.3	524	4	US-09-538-092-1301
20	900	29.1	524	2	US-08-615-942A-2
21	900	29.1	524	4	US-09-237-325-2
22	889	29.1	544	3	US-08-559-397A-19
23	884	28.9	506	1	US-08-369-780-2
24	884	28.9	506	1	US-08-475-682-2
25	894	28.9	506	1	US-08-780-833-2
26	894	28.9	506	1	US-08-636-036-2
27	894	28.9	506	3	US-08-918-509-2

28	894	28.9	506	3	US-09-108-262-2	Sequence 2, App1
29	894	28.9	506	4	US-09-688-188B-94	Sequence 94, App1
30	894	28.9	506	4	US-09-291-417D-94	Sequence 94, App1
31	893.5	28.9	551	4	US-09-949-016-10951	Sequence 10951, A
32	892.5	28.9	545	4	US-09-538-092-1297	Sequence 1297, Ap
33	891.5	28.9	545	2	US-08-935-760-4	Sequence 4, App1
34	891.5	28.9	545	4	US-09-688-188B-93	Sequence 93, App1
35	891.5	28.9	545	4	US-09-291-417D-93	Sequence 93, App1
36	867	28.1	544	3	US-08-559-397A-29	Sequence 29, App1
37	849	27.5	544	3	US-08-559-397A-30	Sequence 30, App1
38	833.5	27.0	465	2	US-08-114-555A-2	Sequence 2, App1
39	821	26.6	694	3	US-08-559-397A-31	Sequence 31, App1
40	814.5	26.4	465	3	US-08-559-397A-2	Sequence 2, App1
41	804	26.0	305	4	US-09-765-815-10	Sequence 10, App1
42	782	25.3	793	3	US-09-588-256-10	Sequence 10, App1
43	769	24.9	268	2	US-08-852-743-3	Sequence 3, App1
44	769	24.9	268	3	US-09-185-370-3	Sequence 3, App1
45	755	24.4	410	4	US-09-248-796A-18461	Sequence 18461, A

ALIGNMENTS

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RESULT 1
US-09-082-737-2
; Sequence 2, Application US/09082737
; Patent No. 6013500
; GENERAL INFORMATION:
; APPLICANT: Minden, Audrey
; TITLE OF INVENTION: PAK; A No. 6013500el Gene Encoding A Serine/
; TITLE OF INVENTION: Threonine Kinase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11230
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,737
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-082-737-2

Query Match      100.0%; Score 3090; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MGKRRKRVETISAPSNFEHRVHTGPDHOKXTGLPRQWOSLIESARPKPLVDPACT 60
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DB      1 MGKRRKRVETISAPSNFEHRVHTGPDHOKXTGLPRQWOSLIESARPKPLVDPACT 60
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QY      61 STOPGAPKTIIVGSKAKGALTLILDEFENNSVTSNSLRSDSPPPARAOENGMPEE 120
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Db 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGMEE 120
QY 121 PATTARGGPGKAGSGRPAHSEAGSGSGDRRRAGPEKRPKSSRGSGGPOESSRDKRL 180
Db 121 PATTARGGPGKAGSGRPAHSEAGSGSGDRRRAGPEKRPKSSRGSGGPOESSRDKRL 180
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Db 181 SGPVGTGPAGIAGSAGKLAAGRPNTYPRADTHPSRGAQGEHPDVAFNGPSAGLAI 240
QY 241 QSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVPPEPGRSPQREPORVS 300
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QY 301 HEOPRAALQIYVDDPDPSPSYLDFNFIKIGSGSTGIVCIATVRSAGKLVAVKMDLRKQOR 360
Db 301 HEOPRAALQIYVDDPDPSPSYLDFNFIKIGSGSTGIVCIATVRSAGKLVAVKMDLRKQOR 360
QY 361 ELLENEVIMRDYQHENVNEMVNSYLVGDELMVMEFLGEGALTDIVTHTMNEBOIAAV 420
Db 361 ELLENEVIMRDYQHENVNEMVNSYLVGDELMVMEFLGEGALTDIVTHTMNEBOIAAV 420
QY 421 CLAVIQAALSVLHAQGVIRHDIKSDSILLTHDGRVYKSDFGCAQVSKVPRKSLVGT 480
Db 421 CLAVIQAALSVLHAQGVIRHDIKSDSILLTHDGRVYKSDFGCAQVSKVPRKSLVGT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPPEYFNEPPLKAMKMI RDNLPRRLKNLHK 540
Db 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPPEYFNEPPLKAMKMI RDNLPRRLKNLHK 540
QY 541 VSPSLKGFRLDLVRDPAQRATAELKHPFLAKAGPASIYVLMKRNTR 591
Db 541 VSPSLKGFRLDLVRDPAQRATAELKHPFLAKAGPASIYVLMKRNTR 591

RESULT 2
US-09-688-188B-103
/ Sequence 103, Application US/09688188B
/ Patent No. 6656716
/ GENERAL INFORMATION:
/ APPLICANT: PLOOMMAN, GREGORY
/ APPLICANT: MARTINEZ, RICARDO
/ APPLICANT: WHYTE, DAVID
/ TITLE OF INVENTION: STEZO-RELATED PROTEIN KINASES
/ FILE REFERENCE: 038602/0328
/ CURRENT APPLICATION NUMBER: US/09/688,188B
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: 09/291,417
/ PRIOR FILING DATE: 1999-04-14
/ PRIOR APPLICATION NUMBER: 60/081,784
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 103
/ LENGTH: 591
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-688-188B-103

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKVEISASNFERRVHTGFDHOKFTGLPRQWOSLIRESARRPKPLVDPACT 60
Db 1 MFGKRRKVEISASNFERRVHTGFDHOKFTGLPRQWOSLIRESARRPKPLVDPACT 60
QY 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGMEE 120
Db 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGMEE 120
QY 121 PATTARGGPGKAGSGRPAHSEAGSGSGDRRRAGPEKRPKSSRGSGGPOESSRDKRL 180
Db 121 PATTARGGPGKAGSGRPAHSEAGSGSGDRRRAGPEKRPKSSRGSGGPOESSRDKRL 180

Db 121 PATTARGGPGKAGSGRPAHSEAGSGSGDRRRAGPEKRPKSSRGSGGPOESSRDKRL 180
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Db 181 SGPVGTGPAGIAGSAGKLAAGRPNTYPRADTHPSRGAQGEHPDVAFNGPSAGLAI 240
QY 241 QSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVPPEPGRSPQREPORVS 300
Db 241 QSSSSSRPPTARAGAPSPGVLGPHASEPOLAPACTPAAPAVPPEPGRSPQREPORVS 300
QY 301 HEOPRAALQIYVDDPDPSPSYLDFNFIKIGSGSTGIVCIATVRSAGKLVAVKMDLRKQOR 360
Db 301 HEOPRAALQIYVDDPDPSPSYLDFNFIKIGSGSTGIVCIATVRSAGKLVAVKMDLRKQOR 360
QY 361 ELLENEVIMRDYQHENVNEMVNSYLVGDELMVMEFLGEGALTDIVTHTMNEBOIAAV 420
Db 361 ELLENEVIMRDYQHENVNEMVNSYLVGDELMVMEFLGEGALTDIVTHTMNEBOIAAV 420
QY 421 CLAVIQAALSVLHAQGVIRHDIKSDSILLTHDGRVYKSDFGCAQVSKVPRKSLVGT 480
Db 421 CLAVIQAALSVLHAQGVIRHDIKSDSILLTHDGRVYKSDFGCAQVSKVPRKSLVGT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPPEYFNEPPLKAMKMI RDNLPRRLKNLHK 540
Db 481 WMAPELISRLPYGPEVDIWSLGIWVTEMVDGEPPEYFNEPPLKAMKMI RDNLPRRLKNLHK 540
QY 541 VSPSLKGFRLDLVRDPAQRATAELKHPFLAKAGPASIYVLMKRNTR 591
Db 541 VSPSLKGFRLDLVRDPAQRATAELKHPFLAKAGPASIYVLMKRNTR 591

RESULT 3
US-09-718-032-2
/ Sequence 2, Application US/09718032
/ Patent No. 6667168
/ GENERAL INFORMATION:
/ APPLICANT: The Trustees of Columbia University
/ APPLICANT: Minden, Audrey
/ TITLE OF INVENTION: FAK4, A NOVEL GENE ENDODING A SERINE/THREONINE KINASE
/ FILE REFERENCE: 575/5311-A-PCT-US
/ CURRENT APPLICATION NUMBER: US/09/718,032
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: PCT/US99/11341
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 09/082,737
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 591
/ TYPE: PRT
/ ORGANISM: human
US-09-718-032-2

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFGKRRKVEISASNFERRVHTGFDHOKFTGLPRQWOSLIRESARRPKPLVDPACT 60
Db 1 MFGKRRKVEISASNFERRVHTGFDHOKFTGLPRQWOSLIRESARRPKPLVDPACT 60
QY 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGMEE 120
Db 61 SIOPGAPKTIYVSGKAGDGLTLLDDEFENMSVTRNSLRDSEPPPARAQENGMEE 120
QY 121 PATTARGGPGKAGSGRPAHSEAGSGSGDRRRAGPEKRPKSSRGSGGPOESSRDKRL 180
Db 121 PATTARGGPGKAGSGRPAHSEAGSGSGDRRRAGPEKRPKSSRGSGGPOESSRDKRL 180
QY 181 SGPVGTGPAGIAGSAGKLAAGRPNTYPRADTHPSRGAQGEHPDVAFNGPSAGLAI 240
Db 181 SGPVGTGPAGIAGSAGKLAAGRPNTYPRADTHPSRGAQGEHPDVAFNGPSAGLAI 240

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DB 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPVAPGPPGRSPQREPORVS 300
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QY 361 ELLFNEVIMRDYOHENNVEMNSYLVGDELWVMEFLGALTDIVTTRMNEEQIAAV 420
DB 361 ELLFNEVIMRDYOHENNVEMNSYLVGDELWVMEFLGALTDIVTTRMNEEQIAAV 420
QY 421 CLAVALQALSVLAQGVTHRDIKSDSILTLTHDGRVXKLSDFGCAQVSKEVPRKSLVGTPT 480
DB 421 CLAVALQALSVLAQGVTHRDIKSDSILTLTHDGRVXKLSDFGCAQVSKEVPRKSLVGTPT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVLEWVDEPPYFNEPPLKAMKIRNLPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVLEWVDEPPYFNEPPLKAMKIRNLPRLKNLHK 540
QY 541 VSPSLKGFDRLLVRDPAGATAAELTKHPFLAKAGPPASIVPLMRQNRTR 591
DB 541 VSPSLKGFDRLLVRDPAGATAAELTKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 4
US-09-291-417D-103
; Sequence 103, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-103

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 SIOPGAPKTIIVGSKAKGALTLTLLDEFENMSVTRSNLSLRDSDPPPARAQENGMPEE 120
DB 61 SIOPGAPKTIIVGSKAKGALTLTLLDEFENMSVTRSNLSLRDSDPPPARAQENGMPEE 120
QY 121 PATTAGGPGKASRGFRFAGHSEAGGSGDRRAAGEKPKRSREGSGGQESSRDRLPL 180
DB 121 PATTAGGPGKASRGFRFAGHSEAGGSGDRRAAGEKPKRSREGSGGQESSRDRLPL 180
QY 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRGAQEPHDVAWNGSAGGLAIP 240
DB 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRGAQEPHDVAWNGSAGGLAIP 240
QY 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPVAPGPPGRSPQREPORVS 300
DB 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPVAPGPPGRSPQREPORVS 300
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DB 301 HEQFRAALQLVDPGPPRSYLDNFITKIGSGTICIAATVRSNGKLVAAVKMDLRKQRR 360
QY 361 ELLFNEVIMRDYOHENNVEMNSYLVGDELWVMEFLGALTDIVTTRMNEEQIAAV 420
DB 361 ELLFNEVIMRDYOHENNVEMNSYLVGDELWVMEFLGALTDIVTTRMNEEQIAAV 420
QY 421 CLAVALQALSVLAQGVTHRDIKSDSILTLTHDGRVXKLSDFGCAQVSKEVPRKSLVGTPT 480
DB 421 CLAVALQALSVLAQGVTHRDIKSDSILTLTHDGRVXKLSDFGCAQVSKEVPRKSLVGTPT 480
QY 481 WMAPELISRLPYGPEVDIWSLGIWVLEWVDEPPYFNEPPLKAMKIRNLPRLKNLHK 540
DB 481 WMAPELISRLPYGPEVDIWSLGIWVLEWVDEPPYFNEPPLKAMKIRNLPRLKNLHK 540
QY 541 VSPSLKGFDRLLVRDPAGATAAELTKHPFLAKAGPPASIVPLMRQNRTR 591
DB 541 VSPSLKGFDRLLVRDPAGATAAELTKHPFLAKAGPPASIVPLMRQNRTR 591

RESULT 5
US-09-949-016-6665
; Sequence 6665, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6665
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6665

Query Match 100.0%; Score 3090; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 3e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MFGKRRKRVEISAPSNFEHRVHTGPDHOKFTGLPRQMSLIIESARRPKPLVDPACTT 60
QY 61 SIOPGAPKTIIVGSKAKGALTLTLLDEFENMSVTRSNLSLRDSDPPPARAQENGMPEE 120
DB 61 SIOPGAPKTIIVGSKAKGALTLTLLDEFENMSVTRSNLSLRDSDPPPARAQENGMPEE 120
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DB 121 PATTAGGPGKASRGFRFAGHSEAGGSGDRRAAGEKPKRSREGSGGQESSRDRLPL 180
QY 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRGAQEPHDVAWNGSAGGLAIP 240
DB 181 SGPDVGTPOPGAGLASAKLAAGRPFNTYPRADTDHPSRGAQEPHDVAWNGSAGGLAIP 240
QY 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPVAPGPPGRSPQREPORVS 300
DB 241 QSSSSSRPPTARAGAPSPGVLAGPHASEPOLAPACTPAAPVAPGPPGRSPQREPORVS 300
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DB 301 HEQFRAALQLVDPGPPRSYLDNFITKIGSGTICIAATVRSNGKLVAAVKMDLRKQRR 360

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Db 361 ELLENVAVIMRDYOHENVVEMTNSYLVDGLVMVMEFLGALTDIVTTRMNEEQIAAV 420
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|
QY 421 CLAVLQALSVLHAQVYIHRDIKSDSILLTHDGRVKLSDPFGCAQVSKEVPRKSLVGTPT 480
|
|
|
Db 421 CLAVLQALSVLHAQVYIHRDIKSDSILLTHDGRVKLSDPFGCAQVSKEVPRKSLVGTPT 480
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|
|
QY 481 WMAPELISRLPYGPEVDIVSLGIMVTEMVDGEPYFNEPPLKAMKIRDNLPRLKNLHK 540
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|
|
Db 481 WMAPELISRLPYGPEVDIVSLGIMVTEMVDGEPYFNEPPLKAMKIRDNLPRLKNLHK 540
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|
|
QY 541 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKRONRTR 591
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|
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Db 541 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKRONRTR 591
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RESULT 6
US-09-949-016-7206
/ Sequence 7206, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: C1001307
/ CURRENT APPLICATION NUMBER: US/09/949, 016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 2000-09-08
/ SOFTWARE: RastSeq for Windows Version 4.0
/ SEQ ID NO 7206
/ LENGTH: 620
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-7206
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Query Match 100.0%; Score 3090; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 3,2e-191;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
|
Db 30 MFGRRKKRVEISAPSNFHHVHTGPDHOKTGTGLFRQWQSLIESARPKLVDPACT 60
|
|
|
QY 61 SIQPGAKTIVGSKAKDQALTLIDDEFENMSVTRNSLNRDSPPPARARQENGMPEE 120
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|
|
Db 90 SIQPGAKTIVGSKAKDQALTLIDDEFENMSVTRNSLNRDSPPPARARQENGMPEE 120
|
|
|
QY 121 PATTAGGCGKAGSRFAGSEAGGSDRRRAGPEKRPKSRGSGGPOESSRDRLPL 180
|
|
|
Db 150 PATTAGGCGKAGSRFAGSEAGGSDRRRAGPEKRPKSRGSGGPOESSRDRLPL 180
|
|
|
QY 181 SGPDVGTQPGAGLAKAGRPNTYPRADTDHPSGAGCEPHDVAFNPGPSAGGLAIP 240
|
|
|
Db 210 SGPDVGTQPGAGLAKAGRPNTYPRADTDHPSGAGCEPHDVAFNPGPSAGGLAIP 240
|
|
|
QY 241 QSSSSSSPPTARARABSPGVLGPHASPOLAPACTPAAPAVGPPGPPSPQREPORVS 300
|
|
|
Db 270 QSSSSSSPPTARARABSPGVLGPHASPOLAPACTPAAPAVGPPGPPSPQREPORVS 300
|
|
|
QY 301 HEQFRAALQLVVDPPDSYLDNFYIKIGEGSTGIVCIATVRSSGKLVAVKMDLRQQR 360
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|
|
Db 330 HEQFRAALQLVVDPPDSYLDNFYIKIGEGSTGIVCIATVRSSGKLVAVKMDLRQQR 360
|
|
|
QY 361 ELLENVAVIMRDYOHENVVEMTNSYLVDGLVMVMEFLGALTDIVTTRMNEEQIAAV 420
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|
|
Db 390 ELLENVAVIMRDYOHENVVEMTNSYLVDGLVMVMEFLGALTDIVTTRMNEEQIAAV 420
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QY 421 CLAVLQALSVLHAQVYIHRDIKSDSILLTHDGRVKLSDPFGCAQVSKEVPRKSLVGTPT 480
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|
|
Db 450 CLAVLQALSVLHAQVYIHRDIKSDSILLTHDGRVKLSDPFGCAQVSKEVPRKSLVGTPT 509
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|
|
QY 481 WMAPELISRLPYGPEVDIVSLGIMVTEMVDGEPYFNEPPLKAMKIRDNLPRLKNLHK 540
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|
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Db 510 WMAPELISRLPYGPEVDIVSLGIMVTEMVDGEPYFNEPPLKAMKIRDNLPRLKNLHK 569
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|
|
QY 541 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKRONRTR 591
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Db 570 VSPSLKGFDRLLVDRDPAQRATAELKHPFLAKAGPPASIVPLMKRONRTR 620
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```
RESULT 7
US-09-688-188B-30
/ Sequence 30, Application US/09688188B
/ Patent No. 6656716
/ GENERAL INFORMATION:
/ APPLICANT: PLOMAN, GREGORY
/ APPLICANT: MARTINEZ, RICARDO
/ APPLICANT: WHYTE, DAVID
/ TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
/ FILE REFERENCE: 038602/0328
/ CURRENT APPLICATION NUMBER: US/09/688, 188B
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: 09/291,417
/ PRIOR FILING DATE: 1999-04-14
/ PRIOR APPLICATION NUMBER: 60/081,784
/ PRIOR FILING DATE: 1998-04-14
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 30
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-688-188B-30
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Query Match 67.1%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 5,8e-116;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAARPPNTYPRADTDHPSGAGCEPHDVAFNPGPSAGGLAIPQSSSSSRPPTRA 253
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|
|
Db 1 ASGAKLAARPPNTYPRADTDHPSGAGCEPHDVAFNPGPSAGGLAIPQSSSSSRPPTRA 253
|
|
|
QY 254 RGAPSPGVLGPHASPOLAPACTPAAPAVGPPGPPSPQREPORVSHQFRALQLVVD 313
|
|
|
Db 61 RGAPSPGVLGPHASPOLAPACTPAAPAVGPPGPPSPQREPORVSHQFRALQLVVD 313
|
|
|
QY 314 PGDPPSYLDNFYIKIGEGSTGIVCIATVRSSGKLVAVKMDLRQQRRELLFNEVIMRDY 120
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|
|
Db 121 PGDPPSYLDNFYIKIGEGSTGIVCIATVRSSGKLVAVKMDLRQQRRELLFNEVIMRDY 120
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|
|
QY 374 OHENVVEMTNSYLVDGLVMVMEFLGALTDIVTTRMNEEQIAAVCLAVLQALSVLHA 433
|
|
|
Db 181 OHENVVEMTNSYLVDGLVMVMEFLGALTDIVTTRMNEEQIAAVCLAVLQALSVLHA 433
|
|
|
QY 434 QGVTHRDIKSDSILLTHDGRVKLSDPFGCAQVSKEVPRKSLVGTPTWMAPELISRLPYG 493
|
|
|
Db 241 QGVTHRDIKSDSILLTHDGRVKLSDPFGCAQVSKEVPRKSLVGTPTWMAPELISRLPYG 493
|
|
|
QY 494 PEVDIVSLGIMVTEMVDGEPYFNEPPLKAMKIRDNLPRLKNLHKVSPSLKGFDRLL 553
|
|
|
Db 301 PEVDIVSLGIMVTEMVDGEPYFNEPPLKAMKIRDNLPRLKNLHKVSPSLKGFDRLL 553
|
|
|
QY 554 VRDPAQRATAELKHPFLAKAGPPASIVPLMKRONRTR 591
|
|
|
Db 361 VRDPAQRATAELKHPFLAKAGPPASIVPLMKRONRTR 398
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RESULT 8
US-09-291-417D-30
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; Sequence 30, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STERO-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-30

Query Match      67.1%; Score 2073; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 5,8e-126;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 ASGAKLAAGRPFYTPRADTDHPSRGAQGEPRHVAAPNGSAGGLAIPOSSSSSRPPTA 253
DB 1 ASGAKLAAGRPFYTPRADTDHPSRGAQGEPRHVAAPNGSAGGLAIPOSSSSSRPPTA 60
QY 254 RGAPEGVYGPSPHASEPQLAPACTPAAPAVPGPPGRSPQREPORVSHQFRAALQVLD 313
DB 61 RGAPEGVYGPSPHASEPQLAPACTPAAPAVPGPPGRSPQREPORVSHQFRAALQVLD 120
QY 314 PGDPRSYLDFNFIKIGSGTGVCIATVRSSGKLVAVKQDLRQORRELLFNEVIMRDY 373
DB 121 PGDPRSYLDFNFIKIGSGTGVCIATVRSSGKLVAVKQDLRQORRELLFNEVIMRDY 180
QY 374 QHENVEMNSYIVGELWVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLTA 433
DB 181 QHENVEMNSYIVGELWVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLTA 240
QY 434 QGVYHNDISDSTLLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTYMAPELISRLPYG 493
DB 241 QGVYHNDISDSTLLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTYMAPELISRLPYG 300
QY 494 PEVDIVSLGIMVIEWDGEPPEYNEBPPLKAMKMIKRNLPRLKNLHKVSPSLKGFIDRL 553
DB 301 PEVDIVSLGIMVIEWDGEPPEYNEBPPLKAMKMIKRNLPRLKNLHKVSPSLKGFIDRL 360
QY 554 VRDPAQRATRAELKHPFLAKAGPPASIVPLMRQNT 591
DB 361 VRDPAQRATRAELKHPFLAKAGPPASIVPLMRQNT 398

RESULT 9
US-09-688-188B-29
; Sequence 29, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STERO-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
; LENGTH: 681
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-29

Query Match      47.7%; Score 1473.5; DB 4; Length 681;
Best Local Similarity 48.1%; Pred. No. 4.2e-87;
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

QY 4 KKKRVEISAPNFEHRVHTGPDQHEOKTGTGPRQMSLIESARPKLVNPACTTSIQ 63
DB 5 KKKRVEISAPNFEHRVHTGPDQHEOKTGTGPRQMSLIESARPKLVNPACTTSIQ 63
QY 64 PAPKTIYVSGSKGADGALTLLDEFENMSYRSNSLRDSDPPPARAR----- 112
DB 64 LQPMKTIYVSGSKGADGALTLLDEFENMSYRSNSLRDSDPPPARAR----- 112
QY 113 -----QENGM-----PEBPATTARGCPKAGSRG-- 136
DB 124 TDPDNYLQSPQSERDTPHGLVLSGNGTDPAGHKQMPWPEPQSPRVLPNGLAAKAQSIGPA 183
QY 137 RPAHSEAG--GSGDRRRAPPEKPKSREGSGQPSHDKRPLS-----GP 183
DB 184 EFGASQRCLOGLACIQSSPPGASPPGTNRHGMKAAGKGSSEARPOSLVGSATGRPG 243
QY 184 DVGTPQAGLAAAGKLAAGRPFNTYPRADTDHPSRGAQGEPRHVAAPNGSAGGLAIPOSS 243
DB 244 E-GSPPEKTRBSLKRRLFRSM-FLSTATAPSSSKPEPPQSKPN----- 288
QY 244 SSSSRPP-----TRARGASP--GVLGPHASEPOLAPACTPAAPAVPGPPGRS 291
DB 289 -SFPRPQKDNPSLVAAKQSLPSDQPVGTSPPLTTSIDTSPOKSLRTAPATGQLPGRS 347
QY 292 POREPOR-----VSHQFRAALQVLDPGDPRSYL 321
DB 348 PAGESPRTMAQISTSNLYLPDQPTVAKAGALAGEDTGVTHQFKAALRVNVVQGGPRL 407
QY 322 DNPRIKIGSGTGVCIATVRSSGKLVAVKQDLRQORRELLFNEVIMRDYQHENVEM 381
DB 408 DSVYKIGSGTGVCIATVRSSGKLVAVKQDLRQORRELLFNEVIMRDYQHENVEM 467
QY 382 YNSYVDELWVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLHAQGVTHRDI 441
DB 468 YNSYVDELWVMEFLGGLTDIVTTRNMEBOIAVCLAVLQALSVLHAQGVTHRDI 527
QY 442 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTYMAPELISRLPYG 501
DB 528 KSDSILLTHDGRVKLSDFGCAQVSKEVPRRSKSLVGTPTYMAPELISRLPYG 587
QY 502 GIMVIEWDGEPPEYNEBPPLKAMKMIKRNLPRLKNLHKVSPSLKGFIDRLVRDPAQRA 561
DB 588 GIMVIEWDGEPPEYNEBPPLKAMKMIKRNLPRLKNLHKVSPSLKGFIDRLVRDPAQRA 647
QY 562 TAAELKHPFLAKAGPPASIVPLMRQNT 589
DB 648 TAAELKHPFLAKAGPPASIVPLMRQNT 675

RESULT 10
US-09-291-417D-29
; Sequence 29, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STERO-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 29
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-29

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Query Match      47.7%; Score 1473.5; DB 4; Length 681;
Best Local Similarity 48.1%; Pred. No. 4.2e-87;
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

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QY 4 KRKKRVEISAPSNFEHRTVTGPDQHEQKFTGLPRQMSLIESARPKPLVDPACTISIQ 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   KKKKRPEISAPQNFQHRVHTSPDKGKFGVGLPPQWNTL-DTLRPPKPVVDPSRITRVQ 63
DB 5 KKKKRPEISAPQNFQHRVHTSPDKGKFGVGLPPQWNTL-DTLRPPKPVVDPSRITRVQ 63
QY 64 PGAPKTIIVRSKAKKOGALTLILLDEFENMSVTRNSLRDSDPPPPARAR----- 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   LQPMKTIIVRSKAMPVVDYISGLNDYOKLSVLSNTLRGRSPTRRRRAQSLGLGDEHMA 123
DB 64 LQPMKTIIVRSKAMPVVDYISGLNDYOKLSVLSNTLRGRSPTRRRRAQSLGLGDEHMA 123
QY 113 -----OENGM-----PEEPATTARAGGPGKAGSRG-- 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   TDPMYILOSPOSERTDPHGLYLSGNGGTPAGHKQMPPEQSPRVLPNGLAARAKSLGPA 183
DB 124 TDPMYILOSPOSERTDPHGLYLSGNGGTPAGHKQMPPEQSPRVLPNGLAARAKSLGPA 183
QY 137 RPAHSEAG--GSGDRRRAAGPEKRPKSSREGSGPQESSRDKRPLS-----GP 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   EFQASQRCQLQAGACLOSPPGASPTGTNRHGMKAAGSEARPOSLVGSATGRPGG 243
DB 184 EFQASQRCQLQAGACLOSPPGASPTGTNRHGMKAAGSEARPOSLVGSATGRPGG 243
QY 184 DVGTPQAPGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIPQSS 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   E-GSPSPKTRRESSLKRRLFRSM-FLSTAAATAPSSSKPGPPPOSKFN----- 288
DB 244 E-GSPSPKTRRESSLKRRLFRSM-FLSTAAATAPSSSKPGPPPOSKFN----- 288
QY 244 SSSSRPP-----TRAGABSP--GYLGPHASEPQLAPACTPAAPAVPGPGRS 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   -SSFRPPQKDNPPSLVAKAQLPSDQPVGTFSPLTTSPTSSPKSLRTAPATGQLPGRSS 347
DB 289 -SSFRPPQKDNPPSLVAKAQLPSDQPVGTFSPLTTSPTSSPKSLRTAPATGQLPGRSS 347
QY 292 PQREPQR-----VSHQOPRAALQLVVDPPGDRPSYL 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   PAGESPRTWHAQISTSNLYLPDDPTVAKGALAGEPTGVVTHQFALRMVVDDGDRPLLL 407
DB 348 PAGESPRTWHAQISTSNLYLPDDPTVAKGALAGEPTGVVTHQFALRMVVDDGDRPLLL 407
QY 322 DNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVYIMDYOHENNVEM 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   DSYKIVIGEGSTGIVCIAREKISGRQVAVKMDLRKQORRELLFNEVYIMDYOHFNVEM 467
DB 408 DSYKIVIGEGSTGIVCIAREKISGRQVAVKMDLRKQORRELLFNEVYIMDYOHFNVEM 467
QY 382 YNSYIVGDELWVWMEFLFGALTDIVHTNNEBOIAVCLAVIQAALSVLAQGVIRHDI 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   YKSYIVGDELWVWMEFLFGALTDIVSOVRLNEBOIATVCEAVIQAALAYLAHAGVIRHDI 527
DB 468 YKSYIVGDELWVWMEFLFGALTDIVSOVRLNEBOIATVCEAVIQAALAYLAHAGVIRHDI 527
QY 442 KSDSILLTHDGRVKLSDGFCAGVSKVPRRSKSLVGTPLYMAAPELISRLPYGPEVDIWSL 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   KSDSILLTHDGRVKLSDGFCAGVSKVPRRSKSLVGTPLYMAAPELISRLPYGPEVDIWSL 587
DB 548 KSDSILLTHDGRVKLSDGFCAGVSKVPRRSKSLVGTPLYMAAPELISRLPYGPEVDIWSL 587
QY 502 GIMVIEWMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLLVDPDPAQRA 561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   GIMVIEWMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLLVDPDPAQRA 647
DB 588 GIMVIEWMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLLVDPDPAQRA 647
QY 562 TAAELIKHPFLAKAGPPASIVPLMRNR 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   TAAELIKHPFLAKAGPPASIVPLMRNR 675
DB 648 TAAELIKHPFLAKAGPPASIVPLMRNR 675

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RESULT 11
US-09-949-016-10445
; Sequence 10445, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10445
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10445

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```

Query Match      47.7%; Score 1473.5; DB 4; Length 694;
Best Local Similarity 48.1%; Pred. No. 4.3e-87;
Matches 331; Conservative 69; Mismatches 169; Indels 119; Gaps 12;

```

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QY 4 KRKKRVEISAPSNFEHRTVTGPDQHEQKFTGLPRQMSLIESARPKPLVDPACTISIQ 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   KKKKRPEISAPQNFQHRVHTSPDKGKFGVGLPPQWNTL-DTLRPPKPVVDPSRITRVQ 76
DB 18 KKKKRPEISAPQNFQHRVHTSPDKGKFGVGLPPQWNTL-DTLRPPKPVVDPSRITRVQ 76
QY 64 PGAPKTIIVRSKAKKOGALTLILLDEFENMSVTRNSLRDSDPPPPARAR----- 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   LQPMKTIIVRSKAMPVVDYISGLNDYOKLSVLSNTLRGRSPTRRRRAQSLGLGDEHMA 136
DB 77 LQPMKTIIVRSKAMPVVDYISGLNDYOKLSVLSNTLRGRSPTRRRRAQSLGLGDEHMA 136
QY 113 -----OENGM-----PEEPATTARAGGPGKAGSRG-- 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   TDPMYILOSPOSERTDPHGLYLSGNGGTPAGHKQMPPEQSPRVLPNGLAARAKSLGPA 196
DB 137 TDPMYILOSPOSERTDPHGLYLSGNGGTPAGHKQMPPEQSPRVLPNGLAARAKSLGPA 196
QY 137 RPAHSEAG--GSGDRRRAAGPEKRPKSSREGSGPQESSRDKRPLS-----GP 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   EFQASQRCQLQAGACLOSPPGASPTGTNRHGMKAAGSEARPOSLVGSATGRPGG 256
DB 197 EFQASQRCQLQAGACLOSPPGASPTGTNRHGMKAAGSEARPOSLVGSATGRPGG 256
QY 184 DVGTPQAPGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAENGPAGGLAIPQSS 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   E-GSPSPKTRRESSLKRRLFRSM-FLSTAAATAPSSSKPGPPPOSKFN----- 301
DB 257 E-GSPSPKTRRESSLKRRLFRSM-FLSTAAATAPSSSKPGPPPOSKFN----- 301
QY 244 SSSSRPP-----TRAGABSP--GYLGPHASEPQLAPACTPAAPAVPGPGRS 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   -SSFRPPQKDNPPSLVAKAQLPSDQPVGTFSPLTTSPTSSPKSLRTAPATGQLPGRSS 360
DB 302 -SSFRPPQKDNPPSLVAKAQLPSDQPVGTFSPLTTSPTSSPKSLRTAPATGQLPGRSS 360
QY 292 PQREPQR-----VSHQOPRAALQLVVDPPGDRPSYL 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   PAGESPRTWHAQISTSNLYLPDDPTVAKGALAGEPTGVVTHQFALRMVVDDGDRPLLL 420
DB 361 PAGESPRTWHAQISTSNLYLPDDPTVAKGALAGEPTGVVTHQFALRMVVDDGDRPLLL 420
QY 322 DNFIKIGEGSTGIVCIATVRSSGKLVAVKMDLRKQORRELLFNEVYIMDYOHENNVEM 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   DSYKIVIGEGSTGIVCIAREKISGRQVAVKMDLRKQORRELLFNEVYIMDYOHFNVEM 480
DB 421 DSYKIVIGEGSTGIVCIAREKISGRQVAVKMDLRKQORRELLFNEVYIMDYOHFNVEM 480
QY 382 YNSYIVGDELWVWMEFLFGALTDIVHTNNEBOIAVCLAVIQAALSVLAQGVIRHDI 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   YKSYIVGDELWVWMEFLFGALTDIVSOVRLNEBOIATVCEAVIQAALAYLAHAGVIRHDI 540
DB 481 YKSYIVGDELWVWMEFLFGALTDIVSOVRLNEBOIATVCEAVIQAALAYLAHAGVIRHDI 540
QY 442 KSDSILLTHDGRVKLSDGFCAGVSKVPRRSKSLVGTPLYMAAPELISRLPYGPEVDIWSL 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   KSDSILLTHDGRVKLSDGFCAGVSKVPRRSKSLVGTPLYMAAPELISRLPYGPEVDIWSL 600
DB 541 KSDSILLTHDGRVKLSDGFCAGVSKVPRRSKSLVGTPLYMAAPELISRLPYGPEVDIWSL 600
QY 502 GIMVIEWMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLLVDPDPAQRA 561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   GIMVIEWMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLLVDPDPAQRA 660
DB 601 GIMVIEWMDGEPYPNEPPLKAMKIRDNLPRLKNLHKVPSLSKGLFDRLLVDPDPAQRA 660
QY 562 TAAELIKHPFLAKAGPPASIVPLMRNR 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   TAAELIKHPFLAKAGPPASIVPLMRNR 688
DB 661 TAAELIKHPFLAKAGPPASIVPLMRNR 688

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RESULT 12
US-09-765-815-2
; Sequence 2, Application US/09765815
; Patent No. 6673586
; GENERAL INFORMATION:
; APPLICANT: Balk, Steven
; TITLE OF INVENTION: No. 6673586e1 Steroid Hormone Receptor
; TITLE OF INVENTION: Interacting Protein Kinase
; FILE REFERENCE: 01948/068002

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; CURRENT APPLICATION NUMBER: US/09/765, 815
 ; CURRENT FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: US 66/176, 859
 ; PRIOR FILING DATE: 2000-01-19
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 681
 ; TYPE: PR
 ; ORGANISM: Homo sapiens
 US-09-765-815-2

Query Match 47.6%; Score 1470.5; DB 4; Length 681;
 Best Local Similarity 48.0%; Pred. No. 6,5e-87;
 Matches 330; Conservative 70; Mismatches 169; Indels 119; Gaps 12;

```

QY 4 KKKKVEISAPSEFHRVHTGPDQHEOKTGLPRQWOSLIEESARRPKPLVDPACTISIQ 63
DB 5 KKKKREISAPQFQHRVHTSPDKGKFEVGLPPQMNIL-DTLRRPKPVDPDSRITRVQ 63
QY 64 PGAPKTIYSGKAKDGLTLLLDEFENNVTSNSLRDPPPPARAR----- 112
DB 64 LQPKTKVVRGSAAMPVGVYISGLNDIQKLSVSSNTLGRSPYSRRRAQSLGLGDEHMA 123
QY 113 -----QENGM-----PEEPATTARGGPGKAGSRG-- 136
DB 124 TDDPMYLGSPQSRTPHGLYLSGNGTTPAGHKQMPPEQSRVLPNGLAQAQSLGPA 183
QY 137 RFAGHSBAG--GSGDRRRAAGEKPKSSREGSGGQESRDRLPLS-----GP 183
DB 184 EFGAGQRCLOGLACLOSPPGASPTGTRHGMKAKAKHSEARPOSCLVGSATGRPGG 243
QY 184 DVCTPPQAGLASAKLAAGFPNTYPRADTDHPSRGAQSPHVAHPGSAAGLALPQSS 243
DB 244 E-GSPSPKTRSSLRKRLFFSM-FLSTAAATAPSSSKPPGPPQSKRP----- 288
QY 244 SSSSRPP-----TRAGAPSP--GVLGPASBPQALPACTPAPAPVPPGPPPS 291
DB 289 -SSFRPPQKDNPPSLVAKAQSLSPDQVGTFSPLTTSDDSSPQSLRTAPATQGLFRSS 347
QY 292 POREPOR-----VSHQPRALQLVVDPPGPPSYL 321
DB 348 PAPSPTWHAQISTSNLYLPQDPTVAKGALAGEDTVGTHQKALRMVVDGDPRLLL 407
QY 322 DNFTIKGSEGTGVCIAATVRSAGLVAVKMDLRKQORRELLNEVYIMADYHEVNVEM 381
DB 408 DSIVYKLGESTGTVCIAAREKHSRGVAVKMDLRKQORRELLNEVYIMADYHFNVMEM 467
QY 382 YNSYLVGDELMVMEFLGEGALFDIVTHTRMNEEOIAVCLAVLQALSVLHAQGVIRHDI 441
DB 468 YKNTLVGDELMVMEFLGEGALFDIVSQVRLNEEOIAVCEAVLQALSVLHAQGVIRHDI 527
QY 442 KSDSILLTHDGRVXLSDFGCAQVSKVPRKSLVGTPLYMABELISRLPYGPEVDIWSL 501
DB 528 KSDSILLTHDGRVXLSDFGCAQISKDVPRKSLVGTPLYMAPEVISRLIYATEVDIWSL 587
QY 502 GIMVIMVNDGEPPEYFENPPLKAMKMTIDNLPPLKLNHKSPLSKGFLDRLVDPQAQRA 561
DB 588 GIMVIMVNDGEPPEYFSDSPVQAKMLRDSPPPLKLNHKSPLSKGFLDRLVDPQAQRA 647
QY 562 TAAELKHPFLAKAGPPASIVPLMRQNR 589
DB 648 TAOELDHPFLAQTLGPECLVPLIQLYR 675
  
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RESULT 13
 US-09-082-737-3
 ; Sequence 3, Application US/09082737
 ; Patent No. 6013500
 ; GENERAL INFORMATION:
 ; APPLICANT: Minden, Audrey
 ; TITLE OF INVENTION: PAK4; A No. 6013500el Gene Encoding A Serine/
 ; TITLE OF INVENTION: Threonine Kinase

; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11230
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/082,737
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 250 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-082-737-3

Query Match 41.3%; Score 1277; DB 3; Length 250;
 Best Local Similarity 99.6%; Pred. No. 6e-75;
 Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 324 FIKIGSGTGYICIAATVRSAGLVAVKMDLRKQORRELLNEVYIMADYHEVNVEM 383
DB 1 FIKIGSGTGYICIAATVRSAGLVAVKMDLRKQORRELLNEVYIMADYHEVNVEM 60
QY 384 SYLVGDELMVMEFLGEGALFDIVTHTRMNEEOIAVCLAVLQALSVLHAQGVIRHDI 443
DB 61 SYLVGDELMVMEFLGEGALFDIVTHTRMNEEOIAVCLAVLQALSVLHAQGVIRHDI 120
QY 444 DSILLTHDGRVXLSDFGCAQVSKVPRKSLVGTPLYMABELISRLPYGPEVDIWSL 503
DB 121 DSILLTHDGRVXLSDFGCAQVSKVPRKSLVGTPLYMABELISRLPYGPEVDIWSL 180
QY 504 MTEWVDGEPPEYFENPPLKAMKMTIDNLPPLKLNHKSPLSKGFLDRLVDPQAQRA 563
DB 181 MTEWVDGEPPEYFENPPLKAMKMTIDNLPPLKLNHKSPLSKGFLDRLVDPQAQRA 240
QY 564 AELKHPFLA 573
DB 241 AELKHPFLA 250
  
```

RESULT 14
 US-09-718-032-3
 ; Sequence 3, Application US/09718032
 ; Patent No. 6667168
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of Columbia University
 ; APPLICANT: Minden, Audrey
 ; TITLE OF INVENTION: PAK4; A NOVEL GENE ENCODING A SERINE/THREONINE KINASE
 ; FILE REFERENCE: 575/55311-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/718,032
 ; CURRENT FILING DATE: 2000-11-21
 ; PRIOR APPLICATION NUMBER: PCT/US99/11341
 ; PRIOR FILING DATE: 1999-05-21
 ; PRIOR APPLICATION NUMBER: 09/082,737
 ; PRIOR FILING DATE: 1998-05-21

NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 250
TYPE: PRT
ORGANISM: human
US-09-718-032-3

Query Match 41.3%; Score 1277; DB 4; Length 250;
Best Local Similarity 99.6%; Pred. No. 6e-75;
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 324 FIKIGSGTIGVITAVRSSGKLVAVKMDLRKQORRELFNEVVMRDYOHENVMENY 393
DB 1 FIKIGSGTIGVITAVRSSGKLVAVKMDLRKQORRELFNEVVMRDYOHENVMENY 60
QY 384 SYLVGDELWVMEFLEGALTDIVTHTRNMEQIAAVCLAVLQALSVLHAQGVTHRDIKS 443
DB 61 SYLVGDELWVMEFLEGALTDIVTHTRNMEQIAAVCLAVLQALSVLHAQGVTHRDIKS 120
QY 444 DSIILTHDGRVKLSDFCAQVSKVPRKSLVGTYYMAPELISRLPYGPEVDIWSLGI 503
DB 121 DSIILTHDGRVKLSDFCAQVSKVPRKSLVGTYYMAPELISRLPYGPEVDIWSLGI 180
QY 504 MVTIEWDGEPPYFNEBPPLKAMKIRNDLPPRLKNLHKVSPSLKGFILDRLLVDPAPORATA 563
DB 181 MVTIEWDGEPPYFNEBPPLKAMKIRNDLPPRLKNLHKVSPSLKGFILDRLLVDPAPORATA 240
QY 564 AELLKHPFLA 573
DB 241 AELLKHPFLA 250

RESULT 15
US-08-935-760-2
Sequence 2, Application US/08935760A
Patent No. 5952217
GENERAL INFORMATION:
APPLICANT: Gorman, Jessica A.
APPLICANT: Manly, Susan
TITLE OF INVENTION: Recombinant Yeast Cell and Assay Using Same
FILE REFERENCE: ON0156sequence
CURRENT APPLICATION NUMBER: US/08/935,760A
CURRENT FILING DATE: 1997-09-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 544
TYPE: PRT
ORGANISM: Rattus exulans
US-08-935-760-2

Query Match 29.5%; Score 912; DB 2; Length 544;
Best Local Similarity 35.7%; Pred. No. 4.5e-51;
Matches 210; Conservative 87; Mismatches 166; Indels 126; Gaps 8;

QY 4 KRKKRVEISAPSNFERHVTGPDQHQKPTGLPRQWQSLE-----ESARRPKPLVDP 56
DB 63 KKKRVEISAPSNFERHVTGPDQHQKPTGLPRQWQSLE-----ESARRPKPLVDP 121
QY 57 ACITSIOPGAPKTIIVGSKAKDGLTLILDFENMSVTRNSLNRDSDPPPARAQENG 116
DB 122 -----VUKPYDSKETVNNQKMSFT----- 141
QY 117 MPEEPATYARGGKAGRGFRAGHSEAGGSGDRRRAGPEKRPKSSREGSGGPOSSRD 176
DB 142 -----SGDKSAGGYIAHQ-----SNTKTASEPPLAPVSESEDEEEDD 184
QY 177 KRPLSGPDVGTTPAGLASAKLAAGRPNTYPRADTDHPSRGAQGEPRHDVAPNGSAG 236
DB 185 NEP---PPIAAPPREHTKS-----IYTRSVESIASPA-----APNKEATPP 223
QY 237 LAIPQSSSSSRPPTARCAPSPGVLGPHASEPQLAPACTPAPAPAVPGPPGRSPQREP 296

DB 224 SAENANSSTLYRNTDR-----QRKK 243
QY 297 QRVSHQFRALQLVNDPQDPPRSYLDNFIKIGEGSTIGVITAVRSSGKLVAVKMDLRK 356
DB 244 SKMTDEEILIEKRSIVSGVDPKKYTRPEKIGQGSGLVYVALDIATQGEVAIKOMNLOQ 303
QY 357 QORRELFNEVVMRDYOHENVMENYSLVNGDELWVMEFLEGALTDIVTHTRNMEQ 416
DB 304 QPKKELITNEILVMEKKNPNIVNYLDSYLVGDELWVMEFLEGALTDIVTHTRNMEQ 363
QY 417 IAAVCLAVLQALSVLHAQGVTHRDIKSDSIILTHDGRVKLSDFCAQVSKVPRKSLV 476
DB 364 IAAVCRECLQALDFIHSNQVTHRDIKMDNILLGMDGSVKLTFDFCAQITPEQSKRSTMV 423
QY 477 GTPYMAPELISRLPYGPEVDIWSLGIIVTEMVGEPPYFNEBPPLKAMKIRNDLPPRLK 536
DB 424 GTPYMAPEVVTYRKAYGPKVDIWSLGIIVTEMVGEPPYFNEBPPLKAMKIRNDLPPRLK 483
QY 537 NIKHVSPLKGFILDRLLVDPAPORATAELLKHPFLAKAGPPASTVPLM 585
DB 484 NPERLSAVFRDPLNCLMDVDKRSACKELLQHPFLAKFLSSLTPLI 532

Search completed: March 15, 2005, 11:32:29
Job time : 55.1471 secs